NeWSprinter20

Tue Jul 01 14:59:27 1997

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

Release 2.1D John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jul 1 13:06:26 1997; MasPar time 45.21 Seconds
255.216 Million cell updates/sec

Tabular output not generated.

Title: >US-08-726-211-1
Description: (1-18) from US08726211.seq
Perfect Score: 18
N.A. Sequence: 1 CAGCGTGCGCCATCCTTC 18
Comp: GTCGCACGCGGTAGGAAG

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 887282 seqs, 320523884 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS
1:EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8
9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14
15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20
21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26
27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST32
33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38
39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44
45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50
51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST56
57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST62
63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST68
69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74
75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST80
81:EST81 82:EST82 83:EST83 84:EST84 85:EST85 86:EST86
87:EST87 88:EST88 89:EST89 90:EST90 91:EST91 92:EST92
93:EST93 94:EST94 95:EST95 96:EST96 97:EST97 98:EST98
99:EST99
Database: EST-STS-TWO
100:EST100 101:EST101 102:EST102 103:EST103 104:EST104
105:EST105 106:EST106 107:EST107 108:EST108 109:EST109

110:EST110 111:EST111 112:EST112 113:EST113 114:EST114
115:EST115 116:EST116 117:EST117 118:EST118 119:EST119
120:EST120 121:EST121 122:EST122 123:EST123 124:EST124
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135:EST135 136:EST136 137:EST137 138:EST138 139:EST139
140:EST140 141:EST141 142:EST142 143:EST143 144:EST144
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150:EST150 151:EST151 152:EST152 153:EST153 154:EST154
155:EST155 156:EST156 157:EST157 158:EST158 159:EST159
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170:EST170 171:EST171 172:EST172 173:EST173 174:EST174
175:EST175 176:EST176 177:EST177 178:EST178 179:EST179
180:EST180 181:EST181 182:EST182 183:EST183 184:EST184
185:EST185 186:EST186 187:EST187 188:EST188 189:EST189
190:EST190 191:EST191 192:EST192 193:EST193
Database: EST-STS-THREE
194:STS1 195:STS2 196:STS3 197:STS4 198:STS5 199:STS6
200:STS7 201:STS8 202:STS9 203:STS10 204:STS11 205:STS12
206:ueEST 207:gnEST1 208:gnEST2 209:gnEST3 210:gnEST4
211:gnEST5 212:gnEST6 213:gnEST7 214:gnEST8 215:gnEST9
216:gnEST10 217:gnEST11 218:gnEST12 219:gnEST13
220:gnEST14 221:gnEST15 222:gnEST16 223:gnSTS 224:enEST1
225:enEST2 226:enEST3 227:enEST4 228:enEST5 229:enEST6
230:enEST7 231:enEST8 232:enEST9 233:enEST10 234:enEST11
235:enEST12 236:enEST13 237:enEST14 238:enEST15
239:enEST16 240:enEST17 241:enEST18 242:enEST19
243:enEST20 244:enEST21 245:enEST22 246:enEST23
247:enEST24 248:enEST25 249:enEST26 250:enEST27
251:enSTS

Statistics: Mean 6.072; Variance 1.188; scale 5.113

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
c	1	14	77.8	266	93	MUS77F05	Mouse embryonal carci	4.26e-02
c	2	14	77.8	300	65	HSC2QE011	H. sapiens partial cD	4.26e-02
c	3	14	77.8	448	52	H79390	yu48e02.r1 Homo sapie	4.26e-02
c	4	14	77.8	453	175	W66944	me29d08.r1 Soares mou	4.26e-02
	5	14	77.8	563	211	N95054	zb32c05.s1 Homo sapie	4.26e-02
	6	14	77.8	563	118	N95054	zb32c05.s1 Homo sapie	4.26e-02
	7	14	77.8	638	12	AA005111	zh96g10.r1 Soares fet	4.26e-02
c	8	13	72.2	92	122	R86574	RABEST149M Oryctolagu	8.05e-01
	9	13	72.2	241	218	T93415	lmEST0178 LmLV39cDNA	8.05e-01
	10	13	72.2	241	151	T93415	lmEST0178 LmLV39cDNA	8.05e-01
	11	13	72.2	257	151	T93466	lmEST0236 LmLV39cDNA	8.05e-01
	12	13	72.2	265	151	T93448	lmEST0218 LmLV39cDNA	8.05e-01
	13	13	72.2	265	218	T93448	lmEST0218 LmLV39cDNA	8.05e-01
	14	13	72.2	301	64	HSC26F041	H. sapiens partial cD	8.05e-01
c	15	13	72.2	316	47	CELK127B1R	C.elegans cDNA clone	8.05e-01
c	16	13	72.2	328	243	MMA52315	mb15e05.r1 Soares mou	8.05e-01
c	17	13	72.2	328	10	AA052315	mb15e05.r1 Soares mou	8.05e-01

c	18	13	72.2	330	44	CELK011D1F	C.elegans cDNA clone	8.05e-01
c	19	13	72.2	345	54	H86998	yw15c09.r1 Homo sapie	8.05e-01
	20	13	72.2	350	241	MMA30151	mi25g06.r1 Soares mou	8.05e-01
c	21	13	72.2	354	160	T47853	yb17f04.r1 Homo sapie	8.05e-01
	22	13	72.2	371	123	R89144	yp99f08.r1 Homo sapie	8.05e-01
c	23	13	72.2	396	181	W84983	mf43b09.r1 Soares mou	8.05e-01
	24	13	72.2	399	248	MMAA86816	mm85h10.r1 Stratagene	8.05e-01
	25	13	72.2	402	244	MMA66262	mm41g11.r1 Stratagene	8.05e-01
	26	13	72.2	402	15	AA066262	mm41g11.r1 Stratagene	8.05e-01
c	27	13	72.2	405	151	T93841	ye05e08.r1 Homo sapie	8.05e-01
c	28	13	72.2	412	138	R68970	yi37b11.r1 Homo sapie	8.05e-01
	29	13	72.2	419	89	HUM133G09B	Human fetal brain cDN	8.05e-01
	30	13	72.2	434	136	R64449	yi36g04.r1 Homo sapie	8.05e-01
c	31	13	72.2	444	155	W03227	za35a12.r1 Soares fet	8.05e-01
c	32	13	72.2	444	213	W03227	za35a12.r1 Soares fet	8.05e-01
c	33	13	72.2	450	250	ZM6491	43 vegetative meriste	8.05e-01
c	34	13	72.2	450	145	T70649	43 Zea mays cDNA clon	8.05e-01
	35	13	72.2	468	250	TGA37940	TgESTzy56g12.r1 TgRHc	8.05e-01
	36	13	72.2	469	9	AA048837	mj45b06.r1 Soares mou	8.05e-01
c	37	13	72.2	495	87	N60488	TgESTzy09g12.r1 Toxop	8.05e-01
c	38	13	72.2	495	207	N60488	TgESTzy09g12.r1 Toxop	8.05e-01
	39	13	72.2	498	228	HSA36796	zk29a03.r1 Soares pre	8.05e-01
	40	13	72.2	515	113	N76173	yz30d03.r1 Homo sapie	8.05e-01
	41	13	72.2	515	208	N76173	yz30d03.r1 Homo sapie	8.05e-01
	42	13	72.2	541	249	MMAA97487	mk17f01.r1 Soares mou	8.05e-01
	43	13	72.2	569	234	HSAA446	zn46c11.s1 Stratagene	8.05e-01
c	44	13	72.2	1049	215	W08459	mb50b11.r1 Soares mou	8.05e-01
c	45	13	72.2	1049	163	W08459	mb50b11.r1 Soares mou	8.05e-01

ALIGNMENTS

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RESULT    1
LOCUS       MUS77F05      266 bp    mRNA            EST       04-OCT-1996
DEFINITION  Mouse embryonal carcinoma F9 cell cDNA, 77F05.
ACCESSION   D76820
NID         g1596548
KEYWORDS    EST(expressed sequence tag).
SOURCE      Mus musculus cell_line:F9 cell cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Mus.
REFERENCE   1  (bases 1 to 266)
  AUTHORS   Shimada,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-SEP-1995) to the DDBJ/EMBL/GenBank databases.
            Kazunori Shimada, Research Institute for Microbial Diseases, Osaka
            University, Department of Medical Genetics; 3-1 Yamadaoka, Suita,
            Osaka 565, Japan (E-mail:f61246a@center.osaka-u.ac.jp,
            Tel:06-879-8325, Fax:06-879-8326)
REFERENCE   2  (bases 1 to 266)
  AUTHORS   Nishiguchi,S., Sakuma,R., Nomura,M., Zou,Z., Jearanaisilavong,J.,
            Joh,T., Yasunaga,T. and Shimada,K.
  TITLE     A catalogue of genes in mouse embryonal carcinoma F9 cells
            Identified with expressed sequence tags
  JOURNAL   J. Biochem 119, 749-767 (1996)
FEATURES             Location/Qualifiers
     source          1..266
                     /organism="Mus musculus"
```



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                     /cell_line="F9 cell"
BASE COUNT       69 a      71 c      76 g      47 t       3 others
ORIGIN

  Query Match           77.8%;  Score 14;  DB 93;  Length 266;
  Best Local Similarity  93.8%;  Pred. No. 4.26e-02;
  Matches    15;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    185 aggatggcgcaccctg 200
          ||||||||||||  |||
Cp     16 AGGATGGCGCACGCTG 1


RESULT    2
LOCUS       HSC2QE011     300 bp    RNA             EST       21-SEP-1995
DEFINITION  H. sapiens partial cDNA sequence; clone c-2qe01.
ACCESSION   Z45480
NID         g574694
KEYWORDS    partial cDNA sequence; transcribed sequence fragment.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 300)
  AUTHORS   Genexpress.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-OCT-1994) Genethon, B.P. 60, 91002 Evry Cedex France
            and Genetique Moleculaire et Biologie du developpement, CNRS UPR420
            B.P. 8, 94801 Villejuif Cedex France.E-mail: genexpress@genethon.fr
REFERENCE   2  (bases 1 to 300)
  AUTHORS   Genexpress.
  TITLE     The Genexpress cDNA program
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 300)
  AUTHORS   Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
            Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
            Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
            Sebastiani-Kabaktchis,C. and Tessier,A.
  TITLE     IMAGE: molecular integration of the analysis of the human genome
            and its expression
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
  MEDLINE   95277534
COMMENT     Clone library from B.Soares, Psychiatry Dept. Columbia University
            USA;

            Cloning method: total mRNA was oligo-(dT) primed and directionally
            cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
            vector;
            Sequencing method: single read, full automatic;
            Primer: M13 reverse
            cDNA sequence colinear to mRNA
            Stretch removed: nothing
            Normalization method: Bento Soares, P.N.A.S in press;
            Genexpress library idt: C;
            Genexpress sequence idt: y1c-2qe01;

            No significant homology found with :
            genbank release 83 swissprot release 28.
FEATURES             Location/Qualifiers
     source          1..300
```

```
                     /organism="Homo sapiens"
                     /isolate="muscular atrophy patient"
                     /dev_stage="3 months old"
                     /tissue_type="total brain"
                     /clone_lib="normalized infant brain cDNA"
                     /sex="Female"
BASE COUNT       78 a     77 c     83 g     62 t
ORIGIN

  Query Match           77.8%;  Score 14;  DB 65;  Length 300;
  Best Local Similarity  88.9%;  Pred. No. 4.26e-02;
  Matches    16;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    218 gaaggattgcgcaccctg 235
          ||||||| |||||| |||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    3
LOCUS       H79390        448 bp    mRNA            EST       09-NOV-1995
DEFINITION  yu48e02.r1 Homo sapiens cDNA clone 229370 5'.
ACCESSION   H79390
NID         g1057479
KEYWORDS    EST.
SOURCE      human clone=229370 primer=M13RP1 library=Soares fetal liver spleen
            1NFLS vector=pT7T3D (Pharmacia) with a modified polylinker
            host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver
            and spleen from a 20 week-post conception male fetus. 1st strand
            cDNA was primed with a Pac I - oligo(dT) primer [5'
            AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'], double-stranded
            cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
            I and cloned into the Pac I and Eco RI sites of the modified pT7T3
            vector.  Library went through one round of normalization. Library
            constructed by Bento Soares and M.Fatima Bonaldo.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 448)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 332
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES             Location/Qualifiers
```



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     source          1..448
                     /organism="Homo sapiens"
                     /clone="229370"
     mRNA            <1..>448
BASE COUNT      118 a     93 c    111 g    124 t      2 others
ORIGIN

  Query Match           77.8%;  Score 14;  DB 52;  Length 448;
  Best Local Similarity  88.9%;  Pred. No. 4.26e-02;
  Matches    16;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db     58 gaaggattgcgcaccctg 75
          ||||||| |||||| |||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    4
LOCUS       W66944        453 bp    mRNA            EST       14-JUN-1996
DEFINITION  me29d08.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
            clone 388911 5' similar to PIR:S44218 S44218 testin - mouse [1] ;.
ACCESSION   W66944
NID         g1375887
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
            Murinae; Mus.
REFERENCE   1  (bases 1 to 453)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:240743
            Seq primer: mob.REGA+ET
            High quality sequence stop: 348.
FEATURES             Location/Qualifiers
     source          1..453
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTT
                     T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
                     14.5dpc embryos [total RNA provided by  Minoru Ko, Wayne
                     State Univ., from 2 ]; double-stranded cDNA was ligated to
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                     Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector. Library went through one round of
                     normalization, and was constructed by Bento Soares and
                     M.Fatima Bonaldo."
                     /clone="388911"
                     /clone_lib="Soares mouse embryo NbME13.5 14.5"
                     /sex="unknown"
                     /tissue_type="embryo"
                     /dev_stage="13.5-14.5dpc total fetus"
                     /lab_host="DH10B"
     mRNA            <1..>453
BASE COUNT      111 a    120 c    140 g     82 t
ORIGIN

  Query Match           77.8%;  Score 14;  DB 175;  Length 453;
  Best Local Similarity  88.9%;  Pred. No. 4.26e-02;
  Matches    16;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    333 gaaggatggtgcaccctg 350
          ||||||||| |||| |||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    5
LOCUS       N95054         563 bp    mRNA            EST       09-APR-1996
DEFINITION  zb32c05.s1 Homo sapiens cDNA clone 305288 3' similar to PIR:S44218
            S44218 testin - mouse [1] ;.
ACCESSION   N95054
NID         g1267343
KEYWORDS    EST.
SOURCE      human clone=305288 primer=ETPrimer library=Soares parathyroid tumor
            NbHPA vector=pT7T3D (Pharmacia) with a modified polylinker
            host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI Adult.
            1st strand cDNA was primed with a Not I - oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTTTTTT-
            3'], double-stranded cDNA was size selected, ligated to Eco RI
            adapters (Pharmacia), digested with Not I and cloned into the Not I
            and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library
            went through one round of normalization to a Cot = 5. Library
            constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic
            parathyroid adenomas was kindly provided by Dr. Stephen Marx,
            National Institute of Diabetes and Digestive and Kidney Diseases,
            NIH.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
```



```
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 84
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Possible reversed clone: polyT not found.

            NCBI gi: 1267343
FEATURES              Location/Qualifiers
     source           1..563
                      /organism="Homo sapiens"
                      /clone="305288"
                      /note="human"
     mRNA             <1..>563
BASE COUNT      103 a    159 c    162 g    130 t      9 others
ORIGIN

  Query Match           77.8%;  Score 14;  DB 211;  Length 563;
  Best Local Similarity  88.9%;  Pred. No. 4.26e-02;
  Matches    16;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db     11 cagggtgcaccatccttc 28
          ||| |||| |||||||||
Qy      1 CAGCGTGCGCCATCCTTC 18


RESULT    6
LOCUS       N95054         563 bp    mRNA            EST       09-APR-1996
DEFINITION  zb32c05.s1 Homo sapiens cDNA clone 305288 3' similar to PIR:S44218
            S44218 testin - mouse [1] ;.
ACCESSION   N95054
NID         g1267343
KEYWORDS    EST.
SOURCE      human clone=305288 primer=ETPrimer library=Soares parathyroid tumor
            NbHPA vector=pT7T3D (Pharmacia) with a modified polylinker
            host=DH10B (ampicillin resistant) Rsite1=Not I Rsite2=Eco RI Adult.
            1st strand cDNA was primed with a Not I - oligo(dT) primer
            [5'-TGTTACCAATCTGAAGTGGGAGCGGCCGCACCAATTTTTTTTTTTTTTTTTTTTTTTT-
            3'], double-stranded cDNA was size selected, ligated to Eco RI
            adapters (Pharmacia), digested with Not I and cloned into the Not I
            and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library
            went through one round of normalization to a Cot = 5. Library
            constructed by Bento Soares and M.Fatima Bonaldo. RNA from sporadic
            parathyroid adenomas was kindly provided by Dr. Stephen Marx,
            National Institute of Diabetes and Digestive and Kidney Diseases,
            NIH.
  ORGANISM  Homo sapiens
            Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
            Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
            Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
            Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 563)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
```

```
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 84
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Possible reversed clone: polyT not found.
FEATURES              Location/Qualifiers
     source           1..563
                      /organism="Homo sapiens"
                      /clone="305288"
     mRNA             <1..>563
BASE COUNT      103 a    159 c    162 g    130 t      9 others
ORIGIN

  Query Match           77.8%;  Score 14;  DB 118;  Length 563;
  Best Local Similarity  88.9%;  Pred. No. 4.26e-02;
  Matches    16;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      11 cagggtgcaccatccttc 28
           ||| |||| |||||||||
Qy       1 CAGCGTGCGCCATCCTTC 18


RESULT    7
LOCUS       AA005111      638 bp    mRNA            EST       23-JUL-1996
DEFINITION  zh96g10.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA
            clone 429186 5'.
ACCESSION   AA005111
NID         g1448900
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 638)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
            Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
            Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
            Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
            Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Wilson RK
            WashU-Merck EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
```



```
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: mob.REGA+ET
            High quality sequence stop: 502.
FEATURES              Location/Qualifiers
     source           1..638
                      /organism="Homo sapiens"
                      /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                      with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                      This is a subtracted version of the original Soares fetal
                      liver spleen 1NFLS library.  1st strand cDNA was primed
                      with a Pac I - oligo(dT) primer [5'
                      AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTT 3'],
                      double-stranded cDNA was ligated to Eco RI adaptors
                      (Pharmacia), digested with Pac I and cloned into the Pac I
                      and Eco RI sites of the modified pT7T3 vector.  Library
                      went through one round of normalization. Library
                      constructed by Bento Soares and M.Fatima Bonaldo."
                      /clone="429186"
                      /clone_lib="Soares fetal liver spleen 1NFLS S1"
                      /sex="male"
                      /dev_stage="20 week-post conception fetus"
                      /lab_host="DH10B (ampicillin resistant)"
     mRNA             <1..>638
BASE COUNT      193 a    175 c    135 g    133 t      2 others
ORIGIN

  Query Match           77.8%;  Score 14;  DB 12;  Length 638;
  Best Local Similarity  88.9%;  Pred. No. 4.26e-02;
  Matches    16;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db     553 cagcgtgccccaaccttc 570
           |||||||| ||| |||||
Qy       1 CAGCGTGCGCCATCCTTC 18


RESULT    8
LOCUS       R86574        92 bp    mRNA            EST       02-APR-1996
DEFINITION  RABEST149M Oryctolagus cuniculus cDNA clone pRABOC149 3'.
ACCESSION   R86574
NID         g947228
KEYWORDS    EST.
SOURCE      rabbit clone=pRABOC149 primer=M13 forward library=Rabbit
            Osteoclast, Dennis Sakai strain=New Zealand White vector=pSPORT1
            host=E. coli DH12S Rsite1=SalI Rsite2=NotI Poly(A)+ RNA was
            purified from a 97% pure population of osteoclasts prepared from
            the long bones of 10 day old rabbits.  First strand cDNA was
            synthesized by priming with an oligo(dT)-NotI anchor-primer and
            second strand cDNA was synthesized by replacement synthesis as
            described by Gubler and Hoffman (Gene 25:283, 1983).  Following the
            addition of SalI adapters and NotI digestion, the cDNA was cloned
            between the SalI (5o) and NotI (3o) sites of the pSPORT1 (BRL)
            plasmid vector.
  ORGANISM  Oryctolagus cuniculus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Osteichthyes; Sarcopterygii; Mammalia; Eutheria;
            Lagomorpha; Leporidae; Oryctolagus.
REFERENCE   1  (bases 1 to 92)
  AUTHORS   Sakai,D., Tong,H.-S. and Minkin,C.
  TITLE     Osteoclast Molecular Phenotyping by Random cDNA Sequencing
```

```
  JOURNAL   Bone 17 (2), 111-119 (1995)
  MEDLINE   96021365
COMMENT     Other_ESTs: RABEST149T
            Contact: Sakai D
            Basic Sciences
            University of Southern California
            USC School of Dentistry, 925 West 34th Street, DEN-4220, Los
            Angeles, CA 90089-0641
            Tel: 2137405563
            Fax: 2137407560
            Email: sakai@molbio.usc.edu.
FEATURES             Location/Qualifiers
     source          1..92
                     /organism="Oryctolagus cuniculus"
                     /clone="pRABOC149"
                     /strain="New Zealand White"
     mRNA            <1..>92
BASE COUNT       24 a     23 c     21 g     22 t      2 others
ORIGIN

  Query Match           72.2%;  Score 13;  DB 122;  Length 92;
  Best Local Similarity  88.2%;  Pred. No. 8.05e-01;
  Matches    15;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      62 aaggacggctcacgctg 78
           ||||| ||| |||||||
Cp      17 AAGGATGGCGCACGCTG 1


RESULT    9
LOCUS       T93415        241 bp    mRNA            EST       01-MAY-1996
DEFINITION  lmEST0178 LmLV39cDNA Leishmania major cDNA clone Lm244 5' END.
ACCESSION   T93415
NID         g726588
KEYWORDS    EST.
SOURCE      Leishmania major.
  ORGANISM  Leishmania major
            Eukaryotae; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;
            Trypanosomatidae; Leishmania.
REFERENCE   1  (bases 1 to 241)
  AUTHORS   Ajioka,J.W.
  TITLE     Leishmania major cDNAs
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Ajioka JW
            Laboratory for Parasite Genome Analysis
            Cambridge University
            Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.
            Tel: 01223333923
            Fax: 01223333923
            Email: jajioka@hgmp.mrc.ac.uk
            Seq primer: T3.

            NCBI gi: 726588
FEATURES             Location/Qualifiers
     source          1..241
                     /organism="Leishmania major"
                     /strain="LV39"
                     /note="Vector: Lambda UNIZAP; Site_1: NotI; Site_2: XhoI;
                     Mid or late log promastigotes.Full length : splice leader
```



```
                     oligo used for second strand synthesis, directional
                     cloning NotI at 5' end, XhoI at 3' end."
                     /clone="Lm244"
                     /clone_lib="LmLV39cDNA"
                     /lab_host="XL1-Blue MRF'"
     mRNA            <1..>241
BASE COUNT       48 a     69 c     64 g     60 t
ORIGIN

  Query Match           72.2%;  Score 13;  DB 218;  Length 241;
  Best Local Similarity 100.0%;  Pred. No. 8.05e-01;
  Matches    13;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     164 tgcgccatccttc 176
           |||||||||||||
Qy       6 TGCGCCATCCTTC 18


RESULT   10
LOCUS       T93415        241 bp    mRNA            EST       01-MAY-1996
DEFINITION  lmEST0178 LmLV39cDNA Leishmania major cDNA clone Lm244 5' END.
ACCESSION   T93415
NID         g726588
KEYWORDS    EST.
SOURCE      Leishmania major.
  ORGANISM  Leishmania major
            Eukaryotae; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;
            Trypanosomatidae; Leishmania.
REFERENCE   1  (bases 1 to 241)
  AUTHORS   Ajioka,J.W.
  TITLE     Leishmania major cDNAs
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Ajioka JW
            Laboratory for Parasite Genome Analysis
            Cambridge University
            Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.
            Tel: 01223333923
            Fax: 01223333923
            Email: jajioka@hgmp.mrc.ac.uk
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1..241
                     /organism="Leishmania major"
                     /strain="LV39"
                     /note="Vector: Lambda UNIZAP; Site_1: NotI; Site_2: XhoI;
                     Mid or late log promastigotes.Full length : splice leader
                     oligo used for second strand synthesis, directional
                     cloning NotI at 5' end, XhoI at 3' end."
                     /clone="Lm244"
                     /clone_lib="LmLV39cDNA"
                     /lab_host="XL1-Blue MRF'"
     mRNA            <1..>241
BASE COUNT       48 a     69 c     64 g     60 t
ORIGIN

  Query Match           72.2%;  Score 13;  DB 151;  Length 241;
  Best Local Similarity 100.0%;  Pred. No. 8.05e-01;
  Matches    13;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;
```

```
Db    164 tgcgccatccttc 176
          |||||||||||||
Qy      6 TGCGCCATCCTTC 18


RESULT   11
LOCUS       T93466        257 bp    mRNA            EST       01-MAY-1996
DEFINITION  lmEST0236 LmLV39cDNA Leishmania major cDNA clone Lm443 5' END.
ACCESSION   T93466
NID         g726639
KEYWORDS    EST.
SOURCE      Leishmania major.
  ORGANISM  Leishmania major
            Eukaryotae; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;
            Trypanosomatidae; Leishmania.
REFERENCE   1  (bases 1 to 257)
  AUTHORS   Ajioka,J.W.
  TITLE     Leishmania major cDNAs
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Ajioka JW
            Laboratory for Parasite Genome Analysis
            Cambridge University
            Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.
            Tel: 01223333923
            Fax: 01223333923
            Email: jajioka@hgmp.mrc.ac.uk
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1..257
                     /organism="Leishmania major"
                     /strain="LV39"
                     /note="Vector: Lambda UNIZAP; Site_1: NotI; Site_2: XhoI;
                     Mid or late log promastigotes.Full length : splice leader
                     oligo used for second strand synthesis, directional
                     cloning NotI at 5' end, XhoI at 3' end."
                     /clone="Lm443"
                     /clone_lib="LmLV39cDNA"
                     /lab_host="XL1-Blue MRF'"
     mRNA            <1..>257
BASE COUNT       49 a     75 c     71 g     62 t
ORIGIN

  Query Match           72.2%;  Score 13;  DB 151;  Length 257;
  Best Local Similarity 100.0%;  Pred. No. 8.05e-01;
  Matches    13;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    178 tgcgccatccttc 190
          |||||||||||||
Qy      6 TGCGCCATCCTTC 18


RESULT   12
LOCUS       T93448        265 bp    mRNA            EST       01-MAY-1996
DEFINITION  lmEST0218 LmLV39cDNA Leishmania major cDNA clone Lm390 5' END.
ACCESSION   T93448
NID         g726621
KEYWORDS    EST.
SOURCE      Leishmania major.
  ORGANISM  Leishmania major
            Eukaryotae; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;
```



```
            Trypanosomatidae; Leishmania.
REFERENCE   1  (bases 1 to 265)
  AUTHORS   Ajioka,J.W.
  TITLE     Leishmania major cDNAs
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Ajioka JW
            Laboratory for Parasite Genome Analysis
            Cambridge University
            Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.
            Tel: 01223333923
            Fax: 01223333923
            Email: jajioka@hgmp.mrc.ac.uk
            Seq primer: T3.
FEATURES             Location/Qualifiers
     source          1..265
                     /organism="Leishmania major"
                     /strain="LV39"
                     /note="Vector: Lambda UNIZAP; Site_1: NotI; Site_2: XhoI;
                     Mid or late log promastigotes.Full length : splice leader
                     oligo used for second strand synthesis, directional
                     cloning NotI at 5' end, XhoI at 3' end."
                     /clone="Lm390"
                     /clone_lib="LmLV39cDNA"
                     /lab_host="XL1-Blue MRF'"
     mRNA            <1..>265
BASE COUNT       51 a     78 c     73 g     63 t
ORIGIN

  Query Match           72.2%;  Score 13;  DB 151;  Length 265;
  Best Local Similarity 100.0%;  Pred. No. 8.05e-01;
  Matches    13;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    178 tgcgccatccttc 190
          |||||||||||||
Qy      6 TGCGCCATCCTTC 18


RESULT   13
LOCUS       T93448        265 bp    mRNA            EST       01-MAY-1996
DEFINITION  lmEST0218 LmLV39cDNA Leishmania major cDNA clone Lm390 5' END.
ACCESSION   T93448
NID         g726621
KEYWORDS    EST.
SOURCE      Leishmania major.
  ORGANISM  Leishmania major
            Eukaryotae; mitochondrial eukaryotes; Euglenozoa; Kinetoplastida;
            Trypanosomatidae; Leishmania.
REFERENCE   1  (bases 1 to 265)
  AUTHORS   Ajioka,J.W.
  TITLE     Leishmania major cDNAs
  JOURNAL   Unpublished (1995)
COMMENT
            Contact: Ajioka JW
            Laboratory for Parasite Genome Analysis
            Cambridge University
            Department of Pathology, Tennis Court Road, Cambridge CB2 1QP, UK.
            Tel: 01223333923
            Fax: 01223333923
            Email: jajioka@hgmp.mrc.ac.uk
```

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            Seq primer: T3.

            NCBI gi: 726621
FEATURES              Location/Qualifiers
     source           1..265
                      /organism="Leishmania major"
                      /strain="LV39"
                      /note="Vector: Lambda UNIZAP; Site_1: NotI; Site_2: XhoI;
                      Mid or late log promastigotes.Full length : splice leader
                      oligo used for second strand synthesis, directional
                      cloning NotI at 5' end, XhoI at 3' end."
                      /clone="Lm390"
                      /clone_lib="LmLV39cDNA"
                      /lab_host="XL1-Blue MRF'"
     mRNA             <1..>265
BASE COUNT       51 a     78 c     73 g     63 t
ORIGIN

  Query Match           72.2%;  Score 13;  DB 218;  Length 265;
  Best Local Similarity 100.0%;  Pred. No. 8.05e-01;
  Matches    13;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    178 tgcgccatccttc 190
          |||||||||||||
Qy      6 TGCGCCATCCTTC 18


RESULT   14
LOCUS       HSC26F041     301 bp    RNA             EST       21-SEP-1995
DEFINITION  H. sapiens partial cDNA sequence; clone c-26f04.
ACCESSION   F07460
NID         g673120
KEYWORDS    partial cDNA sequence; transcribed sequence fragment.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 301)
  AUTHORS   Genexpress.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JAN-1995) Genethon, B.P. 60, 91002 Evry Cedex France
            and Genetique Moleculaire et Biologie du developpement, CNRS UPR420
            B.P. 8, 94801 Villejuif Cedex France E-mail: genexpress@genethon.fr
REFERENCE   2  (bases 1 to 301)
  AUTHORS   Genexpress.
  TITLE     The Genexpress cDNA program
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 301)
  AUTHORS   Auffray,C., Behar,G., Bois,F., Bouchier,C., da Silva,C.,
            Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
            Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
            Sebastiani-Kabaktchis,C. and Tessier,A.
  TITLE     IMAGE: molecular integration of the analysis of the human genome
            and its expression
  JOURNAL   C. R. Acad. Sci. III, Sci. Vie 318 (2), 263-272 (1995)
  MEDLINE   95277534
COMMENT     Cloning method: total mRNA was oligo-(dT) primed and directionally
            cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
            vector;
            Sequencing method: single read, full automatic;
```



```
            Primer: M13_reverse
            cDNA sequence colinear to mRNA
            Stretch removed: nothing
            Normalization method: Bento Soares, P.N.A.S. 91:9228-9232(1994);
            Genexpress_library_idt: C;
            Genexpress_sequence_idt: ylc-26f04.
FEATURES              Location/Qualifiers
     source           1..301
                      /organism="Homo sapiens"
                      /isolate="muscular atrophy patient"
                      /clone_lib="normalized infant brain cDNA from B.Soares,
                      Psychiatry Dept. Columbia University USA"
                      /sex="female"
                      /tissue_type="total brain"
                      /dev_stage="3 months old"
BASE COUNT       48 a     90 c     91 g     71 t      1 others
ORIGIN

  Query Match           72.2%;  Score 13;  DB 64;  Length 301;
  Best Local Similarity  93.3%;  Pred. No. 8.05e-01;
  Matches    14;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    188 cgtgagccatccttc 202
          |||| ||||||||||
Qy      4 CGTGCGCCATCCTTC 18


RESULT   15
LOCUS       CELK127B1R    316 bp    mRNA            EST       12-DEC-1995
DEFINITION  C.elegans cDNA clone yk127b1 : 3' end, single read.
ACCESSION   D64881
NID         g1117323
KEYWORDS    EST(expressed sequence tag).
SOURCE      Caenorhabditis elegans (strain CB1489 him-8(e1489), ) (library:
            Yuji kohara unpublished cDNA) Hermaphrodite, male varied whole
            animal cDNA to mRNA.
  ORGANISM  Caenorhabditis elegans
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Nematoda;
            Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea;
            Rhabditidae; Caenorhabditis.
REFERENCE   1  (bases 1 to 316)
  AUTHORS   Kohara,Y., Motohashi,T., Tabara,H., Sugimoto,A., Watanabe,H. and
            Nishigaki,A.
  TITLE     Toward an expression map of the C.elegans genome
  JOURNAL   Unpublished (1995)
COMMENT     Submitted (23-Aug-1995) to DDBJ by:
            Yuji Kohara
            Gene Library Lab.
            National Institute of Genetics
            Yata 1111, Mishima Shizuoka
            411 Japan
            Phone: 0559-81-6854
            Fax  : 0559-81-6855
            Email:ykohara@ddbj.nig.ac.jp.
FEATURES              Location/Qualifiers
     source           1..316
                      /organism="Caenorhabditis elegans"
                      /strain="CB1489 him-8(e1489)"
                      /dev_stage="varied"
                      /sex="Hermaphrodite, male"
```

```
                    /tissue_type="whole animal"
                    /clone_lib="Yuji kohara unpublished cDNA"
BASE COUNT       76 a      65 c      64 g     105 t       6 others
ORIGIN

  Query Match           72.2%;  Score 13;  DB 47;  Length 316;
  Best Local Similarity  93.3%;  Pred. No. 8.05e-01;
  Matches    14;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    183 aagggtggcgcacgc 197
          ||||  ||||||||||
Cp     17 AAGGATGGCGCACGC 3


Search completed: Tue Jul  1 13:14:41 1997
Job time : 495 secs.
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NeWSprinter20

Tue Jul 01 15:00:23 1997

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jul 1 12:58:46 1997; MasPar time 37.84 Seconds
528.936 Million cell updates/sec

Tabular output not generated.

Title: >US-08-726-211-1
Description: (1-18) from US08726211.seq
Perfect Score: 18
N.A. Sequence: 1 CAGCGTGCGCCATCCTTC 18
Comp: GTCGCACGCGGTAGGAAG

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 333249 seqs, 555961234 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: embl-new11
1:BCT 2:FUN 3:GEN 4:HUM1 5:HUM2 6:HUM3 7:INV1 8:INV2
9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM
16:VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC
23:VIR1 24:VIR2

Database: genbank97
25:BCT1 26:BCT2 27:BCT3 28:BCT4 29:BCT5 30:BCT6 31:BCT7
32:BCT8 33:BCT9 34:GEN1 35:GEN2 36:HTG 37:INV1 38:INV2
39:INV3 40:INV4 41:INV5 42:INV6 43:INV7 44:INV8 45:INV9
46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:PAT1
53:PAT2 54:PAT3 55:PAT4 56:PHG 57:PLN1 58:PLN2 59:PLN3
60:PLN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PLN9 66:PLN10
67:PRI1 68:PRI2 69:PRI3 70:PRI4 71:PRI5 72:PRI6 73:PRI7
74:PRI8 75:PRI9 76:PRI10 77:PRI11 78:PRI12 79:PRI13
80:PRI14 81:ROD1 82:ROD2 83:ROD3 84:ROD4 85:ROD5 86:ROD6
87:ROD7 88:ROD8 89:STR 90:SYN 91:UNA 92:VRL1 93:VRL2
94:VRL3 95:VRL4 96:VRL5 97:VRL6 98:VRL7 99:VRL8 100:VRL9

Database: genbank-new11
101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT
107:PHG 108:PLN 109:PRI1 110:PRI2 111:ROD 112:SYN
113:UNA 114:VRL

DSchwartzman 726211

Database: u-embl48_97
115:part1 116:part2

Statistics: Mean 6.349; Variance 2.406; scale 2.639

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description	Pred. No.
c	1	18	100.0	454	80	S72602	bcl2 [human, 697 pre-	5.71e-02
c	2	18	100.0	911	75	HUMBCL2B	Human B-cell leukemia	5.71e-02
c	3	18	100.0	5086	75	HUMBCL2A	Human B-cell leukemia	5.71e-02
c	4	18	100.0	5105	54	I08038	Sequence 1 from Paten	5.71e-02
	5	16	88.9	1708	31	RHMNODD2X	Rhizobium tropici nod	1.85e+00
c	6	16	88.9	1846	70	HSBCL2IG	H.sapiens mRNA for bc	1.85e+00
c	7	15	83.3	1083	101	BHU52149	Borrelia hermsii vari	9.73e+00
c	8	15	83.3	1083	18	BHU52149	Borrelia hermsii vari	9.73e+00
c	9	14	77.8	29	49	CHKC2A101	Chicken alpha-1 type-	4.79e+01
c	10	14	77.8	364	48	S46866	PEC-60=gastrointestin	4.79e+01
c	11	14	77.8	364	48	SSPEC60	S.scrofa PEC-60 mRNA.	4.79e+01
c	12	14	77.8	450	48	SSPBPRNA	S.scrofa mRNA for pla	4.79e+01
	13	14	77.8	700	80	S72412	proteoglycan versican	4.79e+01
c	14	14	77.8	1179	86	RATBCL2A	Rattus norvegicus bcl	4.79e+01
	15	14	77.8	1429	53	A19155	ovine IL-1 beta.	4.79e+01
	16	14	77.8	1930	50	GGCETS2	Chicken mRNA for c-et	4.79e+01
	17	14	77.8	2087	109	HUMPGH3A	Human pgH3 mRNA for p	4.79e+01
	18	14	77.8	2087	78	HUMPGH3A	Human mRNA for proteo	4.79e+01
	19	14	77.8	2155	80	S52488	CSPG2=versican {core	4.79e+01
c	20	14	77.8	2540	27	ECOTOPB	E.coli topoisomerase	4.79e+01
c	21	14	77.8	2914	84	MUSBCL21	Mouse bcl-2 gene enco	4.79e+01
c	22	14	77.8	3204	30	NGU60099	Neisseria gonorrhoeae	4.79e+01
	23	14	77.8	5923	74	HSU26555	Human versican V2 cor	4.79e+01
c	24	14	77.8	5932	41	DROC4A1A	D.melanogaster collag	4.79e+01
c	25	14	77.8	5946	41	DROCOLIV	Drosophila melanogast	4.79e+01
c	26	14	77.8	6030	75	HUMBCL2C	Human bcl-2 mRNA.	4.79e+01
	27	14	77.8	7972	40	DDRN05	Dictyostelium discoid	4.79e+01
	28	14	77.8	8224	75	HSVERS	H.sapiens mRNA for th	4.79e+01
c	29	14	77.8	8541	41	DROCOL4G	Drosophila melanogast	4.79e+01
	30	14	77.8	11185	73	HSU16306	Human chondroitin sul	4.79e+01
	31	14	77.8	12733	25	ATUORF	Agrobacterium rhizoge	4.79e+01
c	32	14	77.8	28888	38	CELC41G11	Caenorhabditis elegan	4.79e+01
c	33	14	77.8	28888	8	CEC41G11	Caenorhabditis elegan	4.79e+01
	34	13	72.2	2425	84	MUSERRMBP	Mouse ecotropic retro	2.20e+02
	35	13	72.2	3529	30	MTU60588	Mycobacterium tubercu	2.20e+02
c	36	13	72.2	4993	19	PP04052	Pseudomonas pickettii	2.20e+02
c	37	13	72.2	5437	31	PSEFUS	P.cepacia fusaric aci	2.20e+02
	38	13	72.2	5651	60	MIPAE7	Podosopora anserina m	2.20e+02
c	39	13	72.2	6492	27	ECODMS	E.coli dmsA, dmsB and	2.20e+02
	40	13	72.2	6892	65	SPURA1	S.pombe mRNA for URA1	2.20e+02
c	41	13	72.2	7391	26	BORVMPPG	Borrelia hermsii rear	2.20e+02
c	42	13	72.2	23349	12	CEZC506	Caenorhabditis elegan	2.20e+02
c	43	13	72.2	23349	39	CEZC506	Caenorhabditis elegan	2.20e+02
	44	13	72.2	36241	30	MLU15186	Mycobacterium leprae	2.20e+02
c	45	13	72.2	100000	36	HSAC000011	EPM1/APECED region of	2.20e+02

ALIGNMENTS

```
RESULT    1
LOCUS       S72602        454 bp    DNA             PRI       10-JUL-1992
DEFINITION  bcl2 [human, 697 pre-B cell acute lymphocytic leukemia cell line,
            Genomic, 454 nt].
ACCESSION   S72602
NID         g241046
KEYWORDS    .
SOURCE      human 697 pre-B cell acute lymphocytic leukemia cell line.
  ORGANISM  Homo sapiens
            Unclassified.
REFERENCE   1  (bases 1 to 454)
  AUTHORS   Tanaka,S., Louie,D.C., Kant,J.A. and Reed,J.C.
  TITLE     Frequent incidence of somatic mutations in translocated BCL2
            oncogenes of non-Hodgkin's lymphomas
  JOURNAL   Blood 79 (1), 229-237 (1992)
  MEDLINE   92096610
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 72602] from the original journal article.
            This sequence comes from Fig.2.
FEATURES             Location/Qualifiers
     source          1..454
                     /organism="Homo sapiens"
     CDS             41..433
                     /partial
                     /gene="bcl2"
                     /codon_start=1
                     /translation="MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAP
                     APGIFSSQPGHTPHPAASRDPVARTSPLQTPAAPGAAAGPALSPVPPVVHLALRQAGD
                     DFSRRYRGDFAEMSSQLHLTPFTARGRFA"
BASE COUNT       65 a    170 c    150 g     69 t
ORIGIN

  Query Match          100.0%;  Score 18;  DB 80;  Length 454;
  Best Local Similarity 100.0%;  Pred. No. 5.71e-02;
  Matches    18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     36 gaaggatggcgcacgctg 53
          ||||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    2
LOCUS       HUMBCL2B      911 bp    mRNA            PRI       31-OCT-1994
DEFINITION  Human B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene mRNA
            encoding bcl-2-beta protein, complete cds.
ACCESSION   M13995
NID         g179368
KEYWORDS    alternative splicing; bcl-2-beta protein; proto-oncogene.
SOURCE      Human pre-B-cell leukemia cell line 380, cDNA to mRNA, clones
            B[15,16]; and DNA, clone lambda-18-27.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 911)
  AUTHORS   Tsujimoto,Y. and Croce,C.M.
  TITLE     Analysis of the structure, transcripts, and protein products of
            bcl-2, the gene involved in human follicular lymphoma
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 83 (14), 5214-5218 (1986)
  MEDLINE   86259760
COMMENT     Clean copy sequence for [1] kindly provided by Y.Tsujimoto,
            10-FEB-1987.  The bcl-2 gene is transcribed by alternative splicing
            into three mRNAs of different sizes.  It consists of at least two
            exons and encodes two proteins which only differ at their
            carboxy-terminal ends, and it is activated by translocation into
            poximity with the Ig heavy chain locus.  Both the normal and
            rearranged bcl-2 gene products are expressed in the B-cell
            leukemia/lymphoma 2 cells.  Genomic clone lambda-18-27 contained
            all the DNA sequences on the 5' of the splice site (position 732).
FEATURES             Location/Qualifiers
     source          1..911
                     /organism="Homo sapiens"
                     /map="18q21.3"
     mRNA            <1..>911
                     /note="bcl2a mRNA"
     CDS             147..764
                     /gene="BCL2"
                     /note="bcl2-beta protein"
                     /codon_start=1
                     /db_xref="GDB:G00-119-031"
                     /db_xref="PID:g179369"
                     /translation="MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAP
                     APGIFSSQPGHTPHPAASRDPVARTSPLQTPAAPGAAAGPALSPVPPVVHLALRQAGD
                     DFSRRYRGDFAEMSSQLHLTPFTARGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVE
                     SVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWVGASGDVSLG"
     misc_feature    732
                     /gene="BCL2"
                     /note="alternative splice donor (intron A start)"
BASE COUNT      156 a    281 c    306 g    168 t
ORIGIN      556 bp upstream of SstI site.

  Query Match          100.0%;  Score 18;  DB 75;  Length 911;
  Best Local Similarity 100.0%;  Pred. No. 5.71e-02;
  Matches    18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    142 gaaggatggcgcacgctg 159
          ||||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    3
LOCUS       HUMBCL2A      5086 bp    mRNA            PRI       31-OCT-1994
DEFINITION  Human B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene mRNA
            encoding bcl-2-alpha protein, complete cds.
ACCESSION   M13994
NID         g179366
KEYWORDS    alternative splicing; bcl-2-alpha protein; proto-oncogene.
SOURCE      Human pre-B-cell leukemia cell line 380, cDNA to mRNA, clones
            B[3,4,10]; and DNA, clone lambda-18-27.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 5086)
  AUTHORS   Tsujimoto,Y. and Croce,C.M.
  TITLE     Analysis of the structure, transcripts, and protein products of
            bcl-2, the gene involved in human follicular lymphoma
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 83 (14), 5214-5218 (1986)
  MEDLINE   86259760
```

```
COMMENT     Clean copy sequence for [1] kindly provided by Y.Tsujimoto,
            10-FEB-1987.
            The bcl-2 gene is transcribed by alternative splicing into three
            mRNAs of different sizes.  It consists of at least two exons and
            encodes two proteins which only differ at their carboxy-terminal
            ends, and it is activated by translocation into poximity with the
            Ig heavy chain locus.  Both the normal and rearranged bcl-2 gene
            products are expressed in the B-cell leukemia/lymphoma 2 cells.
            Genomic clone lambda-18-27 contained all the DNA sequences on the
            5' of the splice site (position 2044).
FEATURES             Location/Qualifiers
     source          1..5086
                     /organism="Homo sapiens"
                     /map="18q21.3"
     mRNA            1..5086
                     /note="bcl2a mRNA"
     CDS             1459..2178
                     /gene="BCL2"
                     /note="bcl2-alpha protein"
                     /codon_start=1
                     /db_xref="GDB:G00-119-031"
                     /db_xref="PID:g179367"
                     /translation="MAHAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAP
                     APGIFSSQPGHTPHPAASRDPVARTSPLQTPAAPGAAAGPALSPVPPVVHLALRQAGD
                     DFSRRYRGDFAEMSSQLHLTPFTARGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVE
                     SVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSMRPLFDFSWLSLK
                     TLLSLALVGACITLGAYLSHK"
BASE COUNT     1262 a    1224 c    1287 g    1313 t
ORIGIN      710 bp upstream of SstI site.

  Query Match          100.0%;  Score 18;  DB 75;  Length 5086;
  Best Local Similarity 100.0%;  Pred. No. 5.71e-02;
  Matches    18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db   1454 gaaggatggcgcacgctg 1471
         ||||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    4
LOCUS       I08038       5105 bp                    PAT       14-NOV-1994
DEFINITION  Sequence 1 from Patent EP 0252685.
ACCESSION   I08038
NID         g589249
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 5105)
  AUTHORS   Tsujimoto,Y. and Croce,C.M.
  TITLE     Diagnostic methods for detecting lymphomas in humans
  JOURNAL   Patent: EP 0252685-A2 1 13-JAN-1988;

FEATURES             Location/Qualifiers
     source          1..5105
                     /organism="unknown"
BASE COUNT     1281 a    1224 c    1287 g    1313 t
ORIGIN

  Query Match          100.0%;  Score 18;  DB 54;  Length 5105;
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```
  Best Local Similarity 100.0%;  Pred. No. 5.71e-02;
  Matches    18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db   1454 gaaggatggcgcacgctg 1471
         ||||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    5
LOCUS       RHMNODD2X    1708 bp    DNA             BCT       09-MAR-1993
DEFINITION  Rhizobium tropici nodulation protein D (nodD2) gene, complete cds.
ACCESSION   L01272
NID         g152365
KEYWORDS    nodD gene; nodulation protein D; regulatory protein.
SOURCE      Rhizobium tropici (strain BR816) DNA.
  ORGANISM  Rhizobium tropici
            Eubacteria; Proteobacteria; alpha subdivision; Rhizobiaceae;
            Rhizobium.
REFERENCE   1  (bases 1 to 1708)
  AUTHORS   van Rhijn,P.J.S., Feys,B. and Vanderleyden,J.
  TITLE     Multiple copies of nodD in Rhizobium tropici CIAT899 and BR816
  JOURNAL   J. Bacteriol. 175, 438-447 (1993)
  MEDLINE   93123162
FEATURES             Location/Qualifiers
     source          1..1708
                     /organism="Rhizobium tropici"
                     /strain="BR816"
     CDS             435..1379
                     /gene="nodD2"
                     /note="putative"
                     /codon_start=1
                     /function="regulatory protein"
                     /product="nodulation protein D"
                     /db_xref="PID:g152366"
                     /transl_table=11
                     /translation="MRFKGLDLNLLVVLDALMTERNLTAAARSINLSQPAMSAAVARL
                     RTNFRDDLFAMAGREFIPTPRAEGLAPAVRDALLQIQLSIVSWEPFNPAQSDRRFRIV
                     LSDYVTLVFFEKVVARAAQEAPGISFDCLPLADDFEELLRRGDIDFLIMPELFMSMHP
                     HAALFEDKFVCVGCRTNEQLSEPFTFERYMSMGHVAVKFGNTRRPTIEEWYLLEHGLK
                     RRIEVVVQGFSMIPPMLSGTERIGTMPLRLAQHFAKTIPLRIVELPLPIPPLAEAVQW
                     PALHNSDPASLWMRELLLQEASLMVSPRAPVRLSAPGF"
     misc_binding    495..558
                     /gene="nodD2"
                     /note="putative"
                     /function="transcription regulation"
                     /bound_moiety="helix-turn-helix DNA-binding"
BASE COUNT      325 a    472 c    488 g    423 t
ORIGIN

  Query Match          88.9%;  Score 16;  DB 31;  Length 1708;
  Best Local Similarity  94.4%;  Pred. No. 1.85e+00;
  Matches    17;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   1612 cagcttgcgccatccttc 1629
         |||| |||||||||||||
Qy      1 CAGCGTGCGCCATCCTTC 18


RESULT    6
LOCUS       HSBCL2IG     1846 bp    RNA             PRI       26-MAR-1993
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DEFINITION  H.sapiens mRNA for bcl2-Ig fusion gene.
ACCESSION   X06487
NID         g288447
KEYWORDS    bcl2-Ig fusion gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1846)
  AUTHORS   Seto,M., Jaeger,U., Hockett,R.D., Graninger,W., Bennett,S.,
            Goldman,P. and Korsmeyer,S.J.
  TITLE     Alternative promoters and exons, somatic mutation and deregulation
            of the Bcl-2-Ig fusion gene in lymphoma
  JOURNAL   EMBO J. 7 (1), 123-131 (1988)
  MEDLINE   88196071
FEATURES             Location/Qualifiers
     source          1..1846
                     /organism="Homo sapiens"
     CDS             887..1606
                     /gene="bcl2-Ig fusion gene"
                     /codon_start=1
                     /db_xref="PID:g288448"
                     /translation="MAHAGRSGYDNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAP
                     APGFFSSQPGHTPHPAASRDPVARTSPLQTPAAPGAAAGPALSPVPPVVHLTLRQAGD
                     DFSRRYRRDFAEMSSQLHLTPFTARGCFATVVEELFRDGVNWGRIVAFFEFGGVMCVE
                     SVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSMRPLFDFSWLSLK
                     TLLSLALVGACITLGAYLGHK"
BASE COUNT      424 a    520 c    483 g    419 t
ORIGIN

  Query Match           88.9%;  Score 16;  DB 70;  Length 1846;
  Best Local Similarity  94.4%;  Pred. No. 1.85e+00;
  Matches    17;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    882 gagggatggcgcacgctg 899
          || ||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    7
LOCUS       BHU52149     1083 bp    DNA             BCT       01-NOV-1996
DEFINITION  Borrelia hermsii variable major protein 18 (vmp18) gene, complete
            cds.
ACCESSION   U52149
NID         g1654227
KEYWORDS    .
SOURCE      Borrelia hermsii strain=HS1; ATCC 35209.
  ORGANISM  Borrelia hermsii
            Eubacteria; Spirochaetales; Spirochaetaceae; Borrelia.
REFERENCE   1  (bases 1 to 1083)
  AUTHORS   Restrepo,B.I., Carter,C.J., Infante,D. and Barbour,A.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-MAR-1996) Alan G. Barbour, Microbiology, UTHSCSA,
            7703 Floyd Curl Drive, San Antonio, TX 78284, USA
FEATURES             Location/Qualifiers
     source          1..1083
                     /organism="Borrelia hermsii"
                     /strain="HS1; ATCC 35209"
     CDS             1..1083
                     /gene="vmp18"
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```
                     /note="VMP18; outer membrane lipoprotein in antigenic
                     variation during relapsing fever; Method: conceptual
                     translation supplied by author"
                     /codon_start=1
                     /product="variable major protein 18"
                     /db_xref="PID:g1654228"
                     /transl_table=11
                     /translation="MRKRISAIINKLNISIMMMIVVLMIGCGQQAVEAGKDGARAATG
                     GRSLSEVLMEVGKSAENAFYSFMALVSDTLGLRVTKDTKKNEVGGYFNSLGGKLGKAS
                     DELEEVAKKSEVEGAKDGPIAVAIRAAVDTAKTTLSTLKGHLESLKGIGDDKVVGWAE
                     NDQQGIKPADDGLNKFLNALQSIVKAATDAGVLAPKAGNTTLTVNGVDNKDGAKVLAI
                     DKPGAAVGEKASLIVSAVSGEEILASIVASKEGDQALGAAADGTTTAMSFAKGGTKDN
                     LSNANTPKAAAVAGGIALRSLVKDGKLASHNDNSEKAVQAAGVIAANKLLVSVEDLIK
                     KTVKNVLEKAKEKIDKARAPKATGQQ"
BASE COUNT      440 a    137 c    270 g    236 t
ORIGIN

  Query Match           83.3%;  Score 15;  DB 101;  Length 1083;
  Best Local Similarity 100.0%;  Pred. No. 9.73e+00;
  Matches    15;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    105 gaaggatggcgcacg 119
          |||||||||||||||
Cp     18 GAAGGATGGCGCACG 4


RESULT    8
ID   BHU52149   standard; DNA; PRO; 1083 BP.
AC   U52149;
NI   g1654227
DT   01-NOV-1996 (Rel. 49, Created)
DT   01-NOV-1996 (Rel. 49, Last updated, Version 1)
DE   Borrelia hermsii variable major protein 18 (vmp18) gene, complete
DE   cds.
KW   .
OS   Borrelia hermsii
OC   Prokaryota; Bacteria; Gracilicutes; Scotobacteria; Spirochetes;
OC   Spirochaetales; Spirochaetaceae.
RN   [1]
RP   1-1083
RA   Restrepo B.I., Carter C.J., Infante D., Barbour A.G.;
RT   ;
RL   Submitted (22-MAR-1996) to the EMBL/GenBank/DDBJ databases.
RL   Alan G. Barbour, Microbiology, UTHSCSA, 7703 Floyd Curl Drive, San
RL   Antonio, TX 78284, USA
FH   Key             Location/Qualifiers
FH
FT   source          1..1083
FT                   /organism="Borrelia hermsii"
FT                   /strain="HS1; ATCC 35209"
FT   CDS             1..1083
FT                   /gene="vmp18"
FT                   /note="VMP18; outer membrane lipoprotein in antigenic
FT                   variation during relapsing fever; Method: conceptual
FT                   translation supplied by author"
FT                   /codon_start=1
FT                   /product="variable major protein 18"
FT                   /transl_table=11
FT                   /db_xref="PID:g1654228"
FT                   /translation="MRKRISAIINKLNISIMMMIVVLMIGCGQQAVEAGKDGARAATG
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FT                   RSLSEVLMEVGKSAENAFYSFMALVSDTLGLRVTKDTKKNEVGGYFNSLGGKLGKASD
  E
FT                   LEEVAKKSEVEGAKDGPIAVAIRAAVDTAKTTLSTLKGHLESLKGIGDDKVVGWAEND
  Q
FT                   QGIKPADDGLNKFLNALQSIVKAATDAGVLAPKAGNTTLTVNGVDNKDGAKVLAIDKP
  G
FT                   AAVGEKASLIVSAVSGEEILASIVASKEGDQALGAAADGTTTAMSFAKGGTKDNLSNA
  N
FT                   TPKAAAVAGGIALRSLVKDGKLASHNDNSEKAVQAAGVIAANKLLVSVEDLIKKTVKN
  V
FT                   LEKAKEKIDKARAPKATGQQ"
SQ   Sequence 1083 BP; 440 A; 137 C; 270 G; 236 T; 0 other;

  Query Match           83.3%;  Score 15;  DB 18;  Length 1083;
  Best Local Similarity 100.0%;  Pred. No. 9.73e+00;
  Matches    15;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    105 gaaggatggcgcacg 119
          |||||||||||||||
Cp     18 GAAGGATGGCGCACG 4


RESULT    9
LOCUS       CHKC2A101      29 bp    DNA             VRT       23-MAY-1996
DEFINITION  Chicken alpha-1 type-II collagen gene; amino acids 578 to 585.
ACCESSION   K02260
NID         g211336
KEYWORDS    alpha-1 type II collagen; collagen.
SEGMENT     1 of 6
SOURCE      Gallus gallus (clone:  LgCOL(II).) DNA.
  ORGANISM  Gallus gallus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Archosauria; Aves; Neognathae; Galliformes;
            Phasianidae; Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 29)
  AUTHORS   Sandell,L.J., Yamada,Y., Dorfman,A. and Upholt,W.B.
  TITLE     Identification of genomic DNA coding for chicken type II
            procollagen
  JOURNAL   J. Biol. Chem. 258 (19), 11617-11621 (1983)
  MEDLINE   84008159
COMMENT     Each procollagen gene codes for the six successive functional
            regions of the protein:  signal peptide, NH-2 propeptide, NH-2
            telopeptide, helical peptide, COOH telopeptide, and COOH
            propeptide.  The type-II COOH-propeptide is cleaved from the
            procollagen molecule after the triple helical molecule is secreted
            into the extracellular matrix.
FEATURES              Location/Qualifiers
     source           1..29
                      /organism="Gallus gallus"
                      /clone="LgCOL(II)."
                      /cell_type="reticulocyte"
     exon             <1..24
                      /note="preprocollagen alpha-1 type-II, AA 578 to 585"
                      /codon_start=1
     intron           25..>29
                      /note="collagen intron"
BASE COUNT        7 a      7 c     11 g      4 t
ORIGIN      Downstream of EcoRI site.
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  Query Match           77.8%;  Score 14;  DB 49;  Length 29;
  Best Local Similarity 100.0%;  Pred. No. 4.79e+01;
  Matches    14;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     10 aaggatggcgcacg 23
          ||||||||||||||
Cp     17 AAGGATGGCGCACG 4


RESULT   10
LOCUS       S46866         364 bp    mRNA            MAM       05-JAN-1993
DEFINITION  PEC-60=gastrointestinal peptide [swine, duodenum, mRNA, 364 nt].
ACCESSION   S46866
NID         g257597
KEYWORDS    .
SOURCE      swine duodenum.
  ORGANISM  Sus sp.
            Unclassified.
REFERENCE   1  (bases 1 to 364)
  AUTHORS   Metsis,M., Cintra,A., Solfrini,V., Ernfors,P., Bortolotti,F.,
            Morrasutti,D.G., Ostenson,C.G., Efendic,S., Agerberth,B., Mutt,V.
            et,al.
  TITLE     Molecular cloning of PEC-60 and expression of its mRNA and peptide
            in the gastrointestinal tract and immune system
  JOURNAL   J. Biol. Chem. 267 (28), 19829-19832 (1992)
  MEDLINE   93015834
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 115614] from the original journal article.
            This sequence comes from Fig. 1.
FEATURES              Location/Qualifiers
     source           1..364
                      /organism="Sus sp."
     CDS              23..283
                      /note="gastrointestinal peptide; Author includes
                      translated amino acids 5' of putative initiation codon;
                      This sequence comes from Fig. 1.  Author-given protein
                      sequence is in conflict with the conceptual translation"
                      /codon_start=1
                      /product="PEC-60"
                      /db_xref="PID:g257598"
                      /translation="RRQPRISMAVRLWVVALALAALFIVDREVPVSAEKQVFSRMPIC
                      EHMTESPDCSRIYDPVCGTDGVTYESECKLCLARIENKQDIQIVKDGEC"
BASE COUNT       91 a     93 c    108 g     72 t
ORIGIN

  Query Match           77.8%;  Score 14;  DB 48;  Length 364;
  Best Local Similarity 88.9%;  Pred. No. 4.79e+01;
  Matches    16;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    265 gaaggatggcgaatgctg 282
          |||||||||||| | ||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT   11
LOCUS       SSPEC60        364 bp    RNA             MAM       06-JUL-1992
DEFINITION  S.scrofa PEC-60 mRNA.
ACCESSION   X67109
NID         g2033
KEYWORDS    pec-60 gene.
```

```
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 364)
  AUTHORS   Metsis,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-JUN-1992) M. Metsis, Dept. of Medical Chemistry, Lab.
            of Molecular Neurobiology, Karolinska Institute, Box 604 00, 10401
            Stockholm, SWEDEN
FEATURES             Location/Qualifiers
     source          1..364
                     /organism="Sus scrofa"
                     /clone_lib="pig duodenum cDNA library in gt10 4x10 6"
     CDS             23..283
                     /evidence=experimental
                     /codon_start=1
                     /product="peptide PEC-60"
                     /db_xref="PID:g2034"
                     /db_xref="SWISS-PROT:P37109"
                     /translation="MAVRLWVVALALAALFIVDREVPVSAEKQVFSRMPICEHMTESP
                     DCSRIYDPVCGTDGVTYESECKLCLARIENKQDIQIVKDGEC"
     sig_peptide     23..76
                     /note="peptide PEC-60"
     mat_peptide     101..280
                     /product="peptide PEC-60"
BASE COUNT       91 a     93 c    108 g     72 t
ORIGIN

  Query Match           77.8%;  Score 14;  DB 48;  Length 364;
  Best Local Similarity  88.9%;  Pred. No. 4.79e+01;
  Matches    16;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    265 gaaggatggcgaatgctg 282
          |||||||||| | ||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT   12
LOCUS       SSPBPRNA      450 bp    RNA             MAM       06-JUL-1994
DEFINITION  S.scrofa mRNA for platelet basic protein.
ACCESSION   X77935
NID         g457753
KEYWORDS    platelet basic protein.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 450)
  AUTHORS   Power,C.A., Proudfoot,A.E., Magnenat,E., Bacon,K.B. and Wells,T.N.
  TITLE     Molecular cloning and characterisation of a neutrophil chemotactic
            protein from porcine platelets
  JOURNAL   Eur. J. Biochem. 221 (2), 713-719 (1994)
  MEDLINE   94229068
REFERENCE   2  (bases 1 to 450)
  AUTHORS   Power,C.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-1994) C.A. Power, Glaxo Institute for Molecular
            Biology, 14 chemin des Aulx, 1228 Plan-les-Ouates, Geneva,
            SWITZERLAND
```



```
FEATURES             Location/Qualifiers
     source          1..450
                     /organism="Sus scrofa"
                     /clone_lib="lambda zapII porcine platelet cDNA library"
     mRNA            <1..450
                     /gene="CTAPIII/NAP-2"
                     /product="platelet basic protein"
     CDS             91..450
                     /gene="CTAPIII/NAP-2"
                     /codon_start=1
                     /product="platelet basic protein"
                     /db_xref="PID:g457754"
                     /db_xref="SWISS-PROT:P43030"
                     /translation="MSLRLGAISSCTTSSPFPVLQVLLPLSLLLTTLVPATMGAAKIE
                     GRMAHVELRCLCLNTVSGIHPSNIQSLEVIRAGAHCAKVEVIATLKNDKKICLDPEAP
                     RIKKIVQKIMEDGGSAA"
     mat_peptide     190..447
                     /gene="CTAPIII/NAP-2"
                     /product="platelet basic protein"
BASE COUNT      110 a    128 c    109 g    103 t
ORIGIN

  Query Match           77.8%;  Score 14;  DB 48;  Length 450;
  Best Local Similarity  88.9%;  Pred. No. 4.79e+01;
  Matches    16;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db    224 gaagaatggcgcacgttg 241
          |||| |||||||||| ||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT   13
LOCUS       S72412        700 bp    mRNA            PRI       28-APR-1995
DEFINITION  proteoglycan versican=large chondroitin sulfate proteoglycan
            (PCR-1) [monkeys, smooth muscle cells, juvenile aorta, mRNA
            Partial, 700 nt].
ACCESSION   S72412
NID         g786543
KEYWORDS    .
SOURCE      monkeys juvenile aorta smooth muscle cells.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   Yao,L.Y., Moody,C., Schonherr,E., Wight,T.N. and Sandell,L.J.
  TITLE     Identification of the proteoglycan versican in aorta and smooth
            muscle cells by DNA sequence analysis, in situ hybridization and
            immunohistochemistry
  JOURNAL   Matrix Biol. 14 (3), 213-225 (1994)
  MEDLINE   95005762
  REMARK    GenBank staff at the National Library of Medicine created this
            entry [NCBI gibbsq 152611] from the original journal article.
            This sequence comes from Fig. 5.
FEATURES             Location/Qualifiers
     source          1..700
                     /organism="unknown"
                     /note="monkeys"
     CDS             1..699
                     /partial
                     /note="Description: proteoglycan versican, CSPG; large
                     chondroitin sulfate proteoglycan; mismatch(50[V->A]); This
```

```
                    sequence comes from Fig. 5.  Author-given protein sequence
                    is in conflict with the conceptual translation"
                    /codon_start=1
                    /product="proteoglycan versican"
                    /db_xref="PID:g786544"
                    /translation="YPIRAPRVGCYGDMMGKAGVRTYGFRSPQETYDVYCYVDHLDGD
                    VFHLTVPSKFTFEEAAKECENQDARLATVGELQAAWRNGFDQCDYGWLSDASVRHPVT
                    VARAQCGGGLLGVRTLYRFENQTGFPPPDSRFDAYCFKRRMSDLSVIGHPIDSESKED
                    EPCSEETDPVHDLMAEILPEFPDIIEIDLYHSEENEEEEEECANATDVTTTPSVQYIN
                    GKHLVTTVPKDPEAA"
BASE COUNT      191 a    155 c    192 g    162 t
ORIGIN

  Query Match           77.8%;  Score 14;  DB 80;  Length 700;
  Best Local Similarity  93.8%;  Pred. No. 4.79e+01;
  Matches    15;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    285 cagcgtgcgccaccct 300
          ||||||||||||| |||
Qy      1 CAGCGTGCGCCATCCT 16


RESULT   14
LOCUS       RATBCL2A     1179 bp    mRNA            ROD       28-NOV-1994
DEFINITION  Rattus norvegicus bcl-2 mRNA, complete cds.
ACCESSION   L14680
NID         g408946
KEYWORDS    bcl-2 gene; dinucleotide repeat; oncogene.
SOURCE      Rattus norvegicus (library: Clontech; TS95-11-2) brain cDNA to
            mRNA.
  ORGANISM  Rattus norvegicus
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;
            Murinae; Rattus.
REFERENCE   1  (bases 1 to 1179)
  AUTHORS   Sato,T., Irie,S., Krajewski,S. and Reed,J.C.
  TITLE     Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein
  JOURNAL   Gene 140 (2), 291-292 (1994)
  MEDLINE   94193015
FEATURES             Location/Qualifiers
     source          1..1179
                     /organism="Rattus norvegicus"
                     /tissue_type="brain"
                     /tissue_lib="Clontech; TS95-11-2"
     CDS             235..945
                     /gene="bcl-2"
                     /codon_start=1
                     /db_xref="PID:g408947"
                     /translation="MAQAGRTGYDNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAP
                     TPGIFSFQPESNRTPAVHRDTAARTSPLRPLVANAGPALSPVPPVVHLTLRRAGDDFS
                     RRYRRDFAEMSSQLHLTPFTARGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVGSVN
                     REMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSMRPLFDFSWLSLKTLL
                     SLALVGACITLGAYLGHK"
     repeat_region   1061..1112
                     /rpt_unit=1061..1062
     polyA_site      1179
BASE COUNT      295 a    316 c    306 g    262 t
ORIGIN

  Query Match           77.8%;  Score 14;  DB 86;  Length 1179;
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```
  Best Local Similarity  93.8%;  Pred. No. 4.79e+01;
  Matches    15;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db    230 gaaggatggcgcaagc 245
          |||||||||||||| ||
Cp     18 GAAGGATGGCGCACGC 3


RESULT   15
LOCUS       A19155       1429 bp    RNA             PAT       09-MAY-1994
DEFINITION  ovine IL-1 beta.
ACCESSION   A19155
NID         g512009
KEYWORDS    .
SOURCE      Ovis sp..
  ORGANISM  Ovis sp.
            Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
            Vertebrata; Eutheria; Artiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Caprinae; Ovis.
REFERENCE   1  (bases 1 to 1429)
  AUTHORS   .
  TITLE     CYTOKINE PRODUCTION
  JOURNAL   Patent: WO 9203574-A 18 05-MAR-1992;

FEATURES             Location/Qualifiers
     source          1..1429
                     /organism="Ovis sp."
     CDS             46..846
                     /codon_start=1
                     /product="ovine IL-1 beta"
                     /db_xref="PID:g512010"
                     /translation="MATVPEPINEVMAYYSDENELLFEVDGPKQMKSCTQHLDLGSMG
                     DGNIQLQISHQLYNKSFRQVVSVIVAMEKLRSRAYEHVFRDDDLRSILSFIFEEEPVI
                     FETSSDELLCDAAVQSVKCKLQDREQKSLVLDSPCVLKALHLLSQEMSREVVFCMSFV
                     QGEERDNKIPVALGIRDKNLYLSCVKKGDTPTLQLEEVDPKVYPKRNMEKRFVFYKTE
                     IKNTVEFESVLYPNWYISTSQIEEKPVFLGRFRGGQDITDFRMETLSP"
BASE COUNT      416 a    363 c    315 g    335 t
ORIGIN

  Query Match           77.8%;  Score 14;  DB 53;  Length 1429;
  Best Local Similarity 100.0%;  Pred. No. 4.79e+01;
  Matches    14;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db   1284 gtgcgccatccttc 1297
          ||||||||||||||
Qy      5 GTGCGCCATCCTTC 18


Search completed: Tue Jul  1 13:05:12 1997
Job time : 386 secs.
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maryh@stic **3147-1**

NeWSprinter20

Tue Jul 01 14:58:39 1997

NeWSprint 2.5 Rev B
Openwin library 3
NeWSprint interpreter 210.0

NeWSprint 2.5

MPSRCH (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Jul 1 13:05:29 1997; MasPar time 5.23 Seconds
318.173 Million cell updates/sec

Tabular output not generated.

Title: >US-08-726-211-1
Description: (1-18) from US08726211.seq
Perfect Score: 18
N.A. Sequence: 1 CAGCGTGCGCCATCCTTC 18
Comp: GTCGCACGCGGTAGGAAG

Scoring table: TABLE default
Gap 10

Nmatch STD : Dbase 0; Query 0

Searched: 121476 seqs, 46255616 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-geneseq26
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 4.967; Variance 2.625; scale 1.892

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
c	1	18	100.0	20	14	Q86649	Bcl-2 translation ini	3.98e-02
	2	18	100.0	22	8	Q49817	Bcl-2 antisense oligo	3.98e-02
	3	18	100.0	22	8	Q49816	Bcl-2 antisense oligo	3.98e-02
c	4	18	100.0	35	14	Q86644	Bcl-2 translation ini	3.98e-02
c	5	18	100.0	765	8	Q49815	Bcl-2.	3.98e-02
c	6	18	100.0	831	1	N81293	Sequence of bcl-2 cDN	3.98e-02
c	7	18	100.0	5086	14	Q86661	Human bcl-2 gene.	3.98e-02
c	8	18	100.0	5086	9	Q54631	Human oncogene bcl-2	3.98e-02
c	9	18	100.0	5105	1	N81292	Sequence of bcl-2 cDN	3.98e-02
c	10	17	94.4	91	9	Q51746	Oligonucleotide probe	1.66e-01
	11	16	88.9	91	9	Q51746	Oligonucleotide probe	6.76e-01
	12	14	77.8	1429	3	Q22825	Sequence encoding ovi	1.02e+01
c	13	14	77.8	1559	10	Q56983	Improved Heat-stable	1.02e+01
c	14	14	77.8	1559	10	Q56981	Improved Heat-stable	1.02e+01
c	15	14	77.8	1559	10	Q56989	Heat-stable carbamyla	1.02e+01
c	16	14	77.8	1559	10	Q56979	Improved Heat-stable	1.02e+01
c	17	14	77.8	1559	10	Q56991	Heat-stable carbamyla	1.02e+01
c	18	14	77.8	1559	10	Q56984	Improved Heat-stable	1.02e+01
c	19	14	77.8	1559	10	Q56980	Improved Heat-stable	1.02e+01
c	20	14	77.8	1559	10	Q56982	Improved Heat-stable	1.02e+01
c	21	14	77.8	1784	10	Q56976	Heat-stable carbamyla	1.02e+01
c	22	14	77.8	1785	10	Q56971	Heat-stable carbamyla	1.02e+01
c	23	14	77.8	1785	10	Q56963	Heat-stable carbamyla	1.02e+01
c	24	14	77.8	1785	10	Q56967	Heat-stable carbamyla	1.02e+01
c	25	14	77.8	1785	10	Q56990	Heat-stable carbamyla	1.02e+01
c	26	14	77.8	1785	10	Q56966	Heat-stable carbamyla	1.02e+01
c	27	14	77.8	1785	10	Q56968	Heat-stable carbamyla	1.02e+01
c	28	14	77.8	1785	10	Q56974	Heat-stable carbamyla	1.02e+01
c	29	14	77.8	1785	10	Q56964	Heat-stable carbamyla	1.02e+01
c	30	14	77.8	1785	10	Q56995	Heat-stable carbamyla	1.02e+01
c	31	14	77.8	1785	10	Q56987	Heat-stable carbamyla	1.02e+01
c	32	14	77.8	1785	4	Q26090	KNK-712.	1.02e+01
c	33	14	77.8	1785	10	Q56986	Heat-stable carbamyla	1.02e+01
c	34	14	77.8	1785	10	Q56970	Heat-stable carbamyla	1.02e+01
c	35	14	77.8	1785	10	Q56994	Heat-stable carbamyla	1.02e+01
c	36	14	77.8	1785	10	Q56969	Heat-stable carbamyla	1.02e+01
c	37	14	77.8	1785	10	Q56978	Heat-stable carbamyla	1.02e+01
c	38	14	77.8	1785	10	Q56972	Heat-stable carbamyla	1.02e+01
c	39	14	77.8	1785	10	Q56992	Heat-stable carbamyla	1.02e+01
c	40	14	77.8	1785	10	Q56977	Heat-stable carbamyla	1.02e+01
c	41	14	77.8	1785	10	Q56975	Heat-stable carbamyla	1.02e+01
c	42	14	77.8	1785	10	Q56988	Heat-stable carbamyla	1.02e+01
c	43	14	77.8	1785	10	Q56973	Heat-stable carbamyla	1.02e+01
c	44	14	77.8	1785	10	Q56965	Heat-stable carbamyla	1.02e+01
	45	14	77.8	8224	2	Q12261	Versican gene.	1.02e+01

ALIGNMENTS

RESULT 1
ID Q86649 standard; DNA; 20 BP.
AC Q86649;
DT 27-SEP-1995 (first entry)
DE Bcl-2 translation initiation site region.
KW Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW lymphoma; programmed cell death; ss.
OS Synthetic.
PN WO9508350-A.
PD 30-MAR-1995.
PF 20-SEP-1994; U10725.
PR 20-SEP-1993; US-124256.
PA (REED/) REED J C.
PI Reed JC;
DR WPI; 95-139394/18.

```
PT   Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT   of human solid tumours, esp. breast cancer
PS   Example 12; Page 33; 108pp; English.
CC   Antisense oligonucleotides were tested for their ability to induce
CC   programmed cell death (DNA fragmentation) in the human lymphoma cell
CC   line RS11846.  The oligonucleotides are phosphodiesters targeted
CC   against the translation initiation site (Q86650-55) or the 5'-cap
CC   region (Q86656-58) of human bcl-2 pre-mRNAs.  A bcl-2 sense sequence
CC   (Q86649) was used as a control.
SQ   Sequence   20 BP;    4 A;    4 C;    10 G;    2 T;

  Query Match          100.0%;  Score 18;  DB 14;  Length 20;
  Best Local Similarity 100.0%;  Pred. No. 3.98e-02;
  Matches    18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      3 gaaggatggcgcacgctg 20
          ||||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    2
ID   Q49817 standard; RNA; 22 BP.
AC   Q49817;
DT   03-MAY-1994  (first entry)
DE   Bcl-2 antisense oligonucleotide.
KW   Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW   expression; myc; ss.
OS   Synthetic.
PN   WO9320200-A.
PD   14-OCT-1993.
PF   02-APR-1993; G00686.
PR   02-APR-1992; GB-007275.
PR   02-APR-1992; GB-007276.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PI   Evan GI;
DR   WPI; 93-336908/42.
PT   Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT   esp. by inhibiting expression of the BCL-2 oncogene e.g. with
PT   antisense oligo:nucleotide(s), also increasing survival of
PT   cultured cells by expressing BCL-2
PS   Disclosure; Page 58; 109pp; English.
CC   A DNA construct comprising the bcl-2 coding sequence under control
CC   of elements allowing its expression is claimed.  Myc-induced cell
CC   death can be inhibited in cultured cells by expressing bcl-2.
CC   Myc-induced cell death can be de-inhibited in tumour cells by admin.
CC   of bcl-2 antisense oligonucleotides.
SQ   Sequence   22 BP;    2 A;    12 C;    4 G;    4 U;

  Query Match          100.0%;  Score 18;  DB 8;  Length 22;
  Best Local Similarity  77.8%;  Pred. No. 3.98e-02;
  Matches    14;  Conservative    4;  Mismatches   0;  Indels   0;  Gaps   0;

Db      3 cagcgugcgccauccuuc 20
          |||||:|||||:||::|
Qy      1 CAGCGTGCGCCATCCTTC 18


RESULT    3
ID   Q49816 standard; DNA; 22 BP.
AC   Q49816;
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```
DT   03-MAY-1994  (first entry)
DE   Bcl-2 antisense oligonucleotide.
KW   Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW   expression; myc; ss.
OS   Synthetic.
PN   WO9320200-A.
PD   14-OCT-1993.
PF   02-APR-1993; G00686.
PR   02-APR-1992; GB-007275.
PR   02-APR-1992; GB-007276.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PI   Evan GI;
DR   WPI; 93-336908/42.
PT   Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT   esp. by inhibiting expression of the BCL-2 oncogene e.g. with
PT   antisense oligo:nucleotide(s), also increasing survival of
PT   cultured cells by expressing BCL-2
PS   Disclosure; Page 58; 109pp; English.
CC   A DNA construct comprising the bcl-2 coding sequence under control
CC   of elements allowing its expression is claimed.  Myc-induced cell
CC   death can be inhibited in cultured cells by expressing bcl-2.
CC   Myc-induced cell death can be de-inhibited in tumour cells by admin.
CC   of bcl-2 antisense oligonucleotides.
SQ   Sequence   22 BP;    2 A;    12 C;    4 G;    4 T;

  Query Match          100.0%;  Score 18;  DB 8;  Length 22;
  Best Local Similarity 100.0%;  Pred. No. 3.98e-02;
  Matches    18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db      3 cagcgtgcgccatccttc 20
          ||||||||||||||||||
Qy      1 CAGCGTGCGCCATCCTTC 18


RESULT    4
ID   Q86644 standard; DNA; 35 BP.
AC   Q86644;
DT   27-SEP-1995  (first entry)
DE   Bcl-2 translation initiation region.
KW   Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW   leukemia; lymphoma; solid tumor; breast cancer; autoimmune disease;
KW   ss.
OS   Synthetic.
PN   WO9508350-A.
PD   30-MAR-1995.
PF   20-SEP-1994; U10725.
PR   20-SEP-1993; US-124256.
PA   (REED/) REED J C.
PI   Reed JC;
DR   WPI; 95-139394/18.
PT   Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT   of human solid tumours, esp. breast cancer
PS   Disclosure; Page 13; 108pp; English.
CC   The antisense oligonucleotide TI-AS (Q86643) straddles the
CC   translation-initiation site in the mRNA coding strand of the human
CC   bcl-2 gene and is complementary to this region.  It reduces the
CC   expression of bcl-2 gene product thereby inducing programmed cell
CC   death of certain cancer cells.  The corresp. sense bcl-1 sequence
CC   was synthesized for use as a control.
SQ   Sequence   35 BP;    6 A;    8 C;    13 G;    8 T;
```

```
  Query Match          100.0%;  Score 18;  DB 14;  Length 35;
  Best Local Similarity 100.0%;  Pred. No. 3.98e-02;
  Matches   18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     13 gaaggatggcgcacgctg 30
          ||||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    5
ID   Q49815 standard; DNA; 765 BP.
AC   Q49815;
DT   03-MAY-1994  (first entry)
DE   Bcl-2.
KW   Cell death; apoptosis; inhibition; de-inhibition; bcl-2 oncogene;
KW   expression; myc; ds.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             31..750
FT   /*tag= a
PN   WO9320200-A.
PD   14-OCT-1993.
PF   02-APR-1993; G00686.
PR   02-APR-1992; GB-007275.
PR   02-APR-1992; GB-007276.
PA   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
PI   Evan GI;
DR   WPI; 93-336908/42.
DR   P-PSDB; R42312.
PT   Treating tumour cells by de-inhibiting Myc-induced apoptosis -
PT   esp. by inhibiting expression of the BCL-2 oncogene e.g. with
PT   antisense oligo:nucleotide(s), also increasing survival of
PT   cultured cells by expressing BCL-2
PS   Claim 26; Page 76-77; 109pp; English.
CC   A DNA construct comprising the bcl-2 coding sequence under control
CC   of elements allowing its expression is claimed.  Myc-induced cell
CC   death can be inhibited in cultured cells by expressing bcl-2.
CC   Myc-induced cell death can be de-inhibited in tumour cells by admin.
CC   of bcl-2 antisense oligonucleotides.
SQ   Sequence   765 BP;    120 A;    251 C;    250 G;    144 T;

  Query Match          100.0%;  Score 18;  DB 8;  Length 765;
  Best Local Similarity 100.0%;  Pred. No. 3.98e-02;
  Matches   18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db     26 gaaggatggcgcacgctg 43
          ||||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    6
ID   N81293 standard; DNA; 831 BP.
AC   N81293;
DT   17-DEC-1990  (first entry)
DE   Sequence of bcl-2 cDNA corresp. to the 3.5 kb transcript encoding
DE   bcl-2-beta
KW   B-cell neoplasm; diagnosis; follicular lymphomas; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
```



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FT   CDS             147..764
FT   /*tag= a
PN   EP-252685-A.
PD   13-JAN-1988.
PF   02-JUL-1987; 305863.
PR   09-JUL-1986; US-883687.
PA   (WIST-) Wistar Corp.
PI   Tsujimoto Y, Croce CM;
DR   WPI; 88-008633/02.
DR   P-PSDB; P80988.
PT   Detection of B-cell neoplasms -
PT   by extn. of proteins or RNA from B-cells and quantitation using
PT   specific antibody or DNA probe
PS   Claim 8; Fig 3; 23pp; English.
CC   Human bcl-2 gene substantially free of introns is claimed. Also claimed
CC   is a substantially pure preparation of a protein having an N-terminal
CC   encoded by the first exon of the human bcl-2 gene the protein being
CC   bcl-2-alpha having about 239 (P80987) or 205 (P80988) residues. B-cell
CC   neoplasms which are associated with t(14;18) chromosome translocations
CC   cause an increase in expression of both the mRNA and the protein prods.
CC   of the bcl-2 gene. This is used to detect B-cell neoplasms including
CC   follicular lymphomas as well as other lymphomas. Bacterial isolates
CC   available as ATCC 67147 and 67148 can be used to express gene prods.
CC   alpha (n81292) and beta (n91293) resp. in bacteria.
SQ   Sequence   831 BP;    138 A;    254 C;    290 G;    149 T;

  Query Match          100.0%;  Score 18;  DB 1;  Length 831;
  Best Local Similarity 100.0%;  Pred. No. 3.98e-02;
  Matches   18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    142 gaaggatggcgcacgctg 159
          ||||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    7
ID   Q86661 standard; DNA; 5086 BP.
AC   Q86661;
DT   27-SEP-1995  (first entry)
DE   Human bcl-2 gene.
KW   Anticode oligomer; antisense oligonucleotide; bcl-2; cancer; therapy;
KW   chemoresistance; ss.
OS   Homo sapiens.
PN   WO9508350-A.
PD   30-MAR-1995.
PF   20-SEP-1994; U10725.
PR   20-SEP-1993; US-124256.
PA   (REED/) REED J C.
PI   Reed JC;
DR   WPI; 95-139394/18.
PT   Anti-code oligomers which bind to bcl-2 mRNA - for the treatment
PT   of human solid tumours, esp. breast cancer
PS   Disclosure; Page 65-68; 108pp; English.
CC   Reversal of chemoresistance of tumor cells by antisense-mediated
CC   reduction of bcl1-2 expression was demonstrated using the
CC   oligonucleotide given in Q86659.  This is antisense to the first
CC   6 codons of the bcl-2 ORF.
SQ   Sequence   5086 BP;    1261 A;    1224 C;    1287 G;    1314 T;

  Query Match          100.0%;  Score 18;  DB 14;  Length 5086;
```

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  Best Local Similarity 100.0%;  Pred. No. 3.98e-02;
  Matches    18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db   1454 gaaggatggcgcacgctg 1471
          ||||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT    8
ID   Q54631 standard; cDNA to mRNA; 5086 BP.
AC   Q54631;
DT   23-JUN-1994  (first entry)
DE   Human oncogene bcl-2 coding sequence.
KW   Cell death; senescence; programmed cell death; ced-9; myocardial
KW   infarction; stroke; brain injury; neurodegenerative disease;
KW   muscular degenerative disease; ageing; hypoxia; ischaemia; toxaemia;
KW   infection; hair loss; neoplasia; cancer; ced-3; ced-4; bcl-2;
KW   oncogene; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1459..2178
FT   /*tag= a
FT   /product= Bcl-2.
PN   WO9325683-A.
PD   23-DEC-1993.
PF   14-JUN-1993; U05651.
PR   12-JUN-1992; US-898933.
PR   10-AUG-1992; US-927681.
PA   (MASI ) MASSACHUSETTS INST TECHNOLOGY.
PI   Hengartner M,  Horvitz HR;
DR   WPI; 94-007540/01.
DR   P-PSDB; R47344.
PT   Caenorhaboitis elegans cell death-protective gene - used to
PT   develop agents for preventing cell death or for reducing
PT   population of cells
PS   Disclosure; Page 61-64; 112pp; English.
CC   The protein product of the human oncogene bcl-2 was found to have a
CC   similar sequence to the ced-9 protein.  ced-9 is essential for
CC   C. elegans development and apparently functions by protecting cells
CC   during development from programmed cell death.  ced-9 was shown to
CC   function by antagonising the activities of cell death genes ced-3
CC   and ced-4.  The ced-9 gene can be used for developing agents for
CC   treating a condtion characterised by increased cell death such as
CC   myocardial infarction, stroke, traumatic brain injury,
CC   neurodegenerative disease, muscular degenerative disease, ageing,
CC   hypoxia, ischaemia, toxaemia, infection or hair loss.  It can also
CC   be used for reducing a population of cells in the treatment of
CC   neoplastic growth cancerous tissue, infected cells or autoreactive
CC   immune cells.
SQ   Sequence   5086 BP;    1262 A;    1222 C;    1288 G;    1314 T;

  Query Match          100.0%;  Score 18;  DB 9;  Length 5086;
  Best Local Similarity 100.0%;  Pred. No. 3.98e-02;
  Matches    18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db   1454 gaaggatggcgcacgctg 1471
          ||||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1
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RESULT    9
ID   N81292 standard; cDNA; 5105 BP.
AC   N81292;
DT   17-DEC-1990  (first entry)
DE   Sequence of bcl-2 cDNA corresp. to the 5.5 kb transcript encoding
DE   bcl-2-alpha
KW   B-cell neoplasm; diagnosis; follicular lymphomas; ss.
OS   Homo sapiens.
FH   Key             Location/Qualifiers
FT   CDS             1459..2178
FT   /*tag= a
PN   EP-252685-A.
PD   13-JAN-1988.
PF   02-JUL-1987; 305863.
PR   09-JUL-1986; US-883687.
PA   (WIST-) Wistar Corp.
PI   Tsujimoto Y, Croce CM;
DR   WPI; 88-008633/02.
DR   P-PSDB; P80987.
PT   Detection of B-cell neoplasms -
PT   by extn. of proteins or RNA from B-cells and quantitation using
PT   specific antibody or DNA probe
PS   Claim 8; Fig 2A-2D; 23pp; English.
CC   A human bcl-2 gene substantially free of introns is claimed. Also claimed
CC   is a substantially pure preparation of a protein having an N-terminal end
CC   encoded by the first exon of the human bcl-2 gene wherein said protein is
CC   bcl-2-alpha having about 239 (P80987) or 205 (P80988) AA residues. B-cell
CC   neoplasms which are associated with t(14;18) chromosome translocations
CC   cause an increase in the expression of both mRNA and the protein prods.
CC   of the bcl-2 gene. This is used to detect B-cell neoplasms including
CC   follicular lymphomas as well as other lymphomas. Bacterial isolates
CC   available as ATCC 67147 and 67148 can be used to express gene prods.
CC   alpha (n81292) and beta (n91293) resp. in bacteria.
SQ   Sequence   5105 BP;    1281 A;    1225 C;    1286 G;    1313 T;

  Query Match          100.0%;  Score 18;  DB 1;  Length 5105;
  Best Local Similarity 100.0%;  Pred. No. 3.98e-02;
  Matches    18;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db   1454 gaaggatggcgcacgctg 1471
          ||||||||||||||||||
Cp     18 GAAGGATGGCGCACGCTG 1


RESULT   10
ID   Q51746 standard; cDNA; 91 BP.
AC   Q51746;
DT   31-MAY-1994  (first entry)
DE   Oligonucleotide probe MK14-A
KW   Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
KW   ss.
OS   Synthetic.
PN   EP-571911-A.
PD   01-DEC-1993.
PF   24-MAY-1993; 108325.
PR   26-MAY-1992; US-889651.
PA   (BECT ) BECTON DICKINSON CO.
PI   Shank DD,  Spears PA;
DR   WPI; 93-378844/48.
PT   New oligo:nucleotide probes specific for Mycobacteria - used for
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PT   detection and amplification of Mycobacteria nucleic acid in
PT   samples
PS   Claim 3; Page 14; 23pp; English.
CC   Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CC   (Q51735).  It hybridized to all spp. of mycobacteria tested, but
CC   cross reacted to a few non-mycobacterial spp.  The probe may
CC   be useful as an initial screen for mycobacterial infection.
CC   See also Q51735-45 and Q51747-59.
SQ   Sequence   91 BP;    5 A;    17 C;    15 G;    4 T;

  Query Match           94.4%;  Score 17;  DB 9;  Length 91;
  Best Local Similarity  0.0%;  Pred. No. 1.66e-01;
  Matches     0;  Conservative   17;  Mismatches   0;  Indels   0;  Gaps   0;

Db      38 svvvvhhvvhvvhhvhy 54
           :::::::::::::::::
Cp      18 GAAGGATGGCGCACGCT 2


RESULT   11
ID   Q51746 standard; cDNA; 91 BP.
AC   Q51746;
DT   31-MAY-1994  (first entry)
DE   Oligonucleotide probe MK14-A
KW   Oligonucleotide; DNA probe; mycobacteria; disease diagnosis;
KW   ss.
OS   Synthetic.
PN   EP-571911-A.
PD   01-DEC-1993.
PF   24-MAY-1993; 108325.
PR   26-MAY-1992; US-889651.
PA   (BECT ) BECTON DICKINSON CO.
PI   Shank DD,  Spears PA;
DR   WPI; 93-378844/48.
PT   New oligo:nucleotide probes specific for Mycobacteria - used for
PT   detection and amplification of Mycobacteria nucleic acid in
PT   samples
PS   Claim 3; Page 14; 23pp; English.
CC   Oligonucleotide probe MK14-A consists of nucleotides 5-95 of MK14
CC   (Q51735).  It hybridized to all spp. of mycobacteria tested, but
CC   cross reacted to a few non-mycobacterial spp.  The probe may
CC   be useful as an initial screen for mycobacterial infection.
CC   See also Q51735-45 and Q51747-59.
SQ   Sequence   91 BP;    5 A;    17 C;    15 G;    4 T;

  Query Match           88.9%;  Score 16;  DB 9;  Length 91;
  Best Local Similarity  0.0%;  Pred. No. 6.76e-01;
  Matches     0;  Conservative   17;  Mismatches   1;  Indels   0;  Gaps   0;

Db      38 svvvvhhvvhvvhhvhyh 55
           ::::::: ::::::::::::
Qy       1 CAGCGTGCGCCATCCTTC 18


RESULT   12
ID   Q22825 standard; DNA; 1429 BP.
AC   Q22825;
DT   22-JUL-1992  (first entry)
DE   Sequence encoding ovine interleukin IL-1beta.
KW   Vaccine; antigen; therapeutic agent; immune response enhancer;
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KW   modulator; ss.
OS   Ovis ammon aries.
FH   Key             Location/Qualifiers
FT   sig_peptide     46..384
FT   /*tag= a
FT   mat_peptide     385..846
FT   /*tag= b
FT   misc_feature    1166..1178
FT   /*tag= c
FT   /label= motif
FT   misc_feature    1194..1203
FT   /*tag= d
FT   /label= motif
FT   misc_feature    1342..1346
FT   /*tag= e
FT   /label= motif
FT   misc_feature    1356..1360
FT   /*tag= f
FT   /label= motif
FT   polyA_signal    1400..1405
FT   /*tag= g
PN   WO9203574-A.
PD   05-MAR-1992.
PF   13-AUG-1991; AU0358.
PR   13-AUG-1990; AU-001698.
PR   11-DEC-1990; AU-003859.
PR   15-FEB-1991; AU-004621.
PR   21-JUN-1991; AU-006840.
PA   (UYME-) UNIV MELBOURNE.
PA   (AWOO ) AUSTRALIAN WOOL CORP.
PI   Brandon MR, Andrews AE, Nash AD, Neeusen EN;
DR   WPI; 92-096916/12.
DR   P-PSDB; R22122.
PT   Nucleotide sequences coding for ruminant cytokine(s) or receptors
PT   - used for producing polypeptide(s) for therapeutic and/or
PT   adjuvant uses in animals
PS   Disclosure; Fig 2A; 93pp; English.
CC   The inventors claim a DNA sequence coding for a polypeptide
CC   exhibiting ruminant cytokine or cytokine receptor activity; ovine
CC   interleukine (IL)-1alpha activity; ovine IL-1alpha activity; ovine
CC   IL-6 activity; ovine tumour nectosis factor (TNF) alpha activity;
CC   ovine IL-2 receptor alpha activity; ovine interferon (IFN)-lambda
CC   activity; or ovine IL-2 activity or homologous sequences, derivs. or
CC   mutants, or fragments.  The recombinant polypeptides are also
CC   claimed.
SQ   Sequence   1429 BP;    416 A;    363 C;    315 G;    335 T;

  Query Match           77.8%;  Score 14;  DB 3;  Length 1429;
  Best Local Similarity 100.0%;  Pred. No. 1.02e+01;
  Matches    14;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Db    1284 gtgcgccatccttc 1297
           ||||||||||||||
Qy       5 GTGCGCCATCCTTC 18


RESULT   13
ID   Q56983 standard; DNA; 1559 BP.
AC   Q56983;
DT   12-AUG-1994  (first entry)
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DE   Improved Heat-stable carbamylase gene.
KW   Decarbamylase; thermal stability; decarbamylation; heat stable;
KW   N-carbamoyl-D-alpha-aminoacid; point mutation; random mutation;
KW   transformant; E.coli; transform; immobilisation; resin; vector; ds.
OS   Agrobacterium radiobacter.
FH   Key             Location/Qualifiers
FT   CDS             4..915
FT   /*tag= a
FT   /product= heat_stable_carbamylase
PN   WO9403613-A.
PD   17-FEB-1994.
PF   05-AUG-1993; J01101.
PR   10-AUG-1992; JP-212692.
PR   21-DEC-1992; JP-340078.
PA   (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.
PI   Ikenaka Y,  Nanba H,  Takahashi S,  Takano M,  Yajima K;
PI   Yamada Y;
DR   WPI; 94-065701/08.
DR   P-PSDB; R46259
PT   DNA coding for a decarbamylase with improved thermal stability -
PT   can be used for decarbamylation of
PT   N-carbamoyl-D-alpha-aminoacid(s)
PS   Claim 18; Page 98-100; 177pp; Japanese.
CC   Sequence (Q56963) shows a DNA encoding a thermal stable decarbamylase.
CC   The enzyme's thermo-stability has been improved by modifing the
CC   decarbamylase gene using 'point' and 'random' mutations. These are
CC   shown in sequences (Q56964-92). Sequences (Q56993-996) are also
CC   improved carbamylases contained within various diffrent vectors for
CC   transformation.
SQ   Sequence   1559 BP;    321 A;    477 C;    465 G;    296 T;

  Query Match           77.8%;  Score 14;  DB 10;  Length 1559;
  Best Local Similarity  93.8%;  Pred. No. 1.02e+01;
  Matches    15;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   1301 aggagggcgcacgctg 1316
          |||| ||||||||||
Cp     16 AGGATGGCGCACGCTG 1


RESULT   14
ID   Q56981 standard; DNA; 1559 BP.
AC   Q56981;
DT   12-AUG-1994  (first entry)
DE   Improved Heat-stable carbamylase gene.
KW   Decarbamylase; thermal stability; decarbamylation; heat stable;
KW   N-carbamoyl-D-alpha-aminoacid; point mutation; random mutation;
KW   transformant; E.coli; transform; immobilisation; resin; vector; ds.
OS   Agrobacterium radiobacter.
FH   Key             Location/Qualifiers
FT   CDS             4..915
FT   /*tag= a
FT   /product= heat_stable_carbamylase
PN   WO9403613-A.
PD   17-FEB-1994.
PF   05-AUG-1993; J01101.
PR   10-AUG-1992; JP-212692.
PR   21-DEC-1992; JP-340078.
PA   (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.
PI   Ikenaka Y,  Nanba H,  Takahashi S,  Takano M,  Yajima K;
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PI   Yamada Y;
DR   WPI; 94-065701/08.
DR   P-PSDB; R46257.
PT   DNA coding for a decarbamylase with improved thermal stability -
PT   can be used for decarbamylation of
PT   N-carbamoyl-D-alpha-aminoacid(s)
PS   Claim 18; Page 92-94; 177pp; Japanese.
CC   Sequence (Q56963) shows a DNA encoding a thermal stable decarbamylase.
CC   The enzyme's thermo-stability has been improved by modifing the
CC   decarbamylase gene using 'point' and 'random' mutations. These are
CC   shown in sequences (Q56964-92). Sequences (Q56993-996) are also
CC   improved carbamylases contained within various diffrent vectors for
CC   transformation.
SQ   Sequence   1559 BP;    321 A;    477 C;    465 G;    296 T;

  Query Match           77.8%;  Score 14;  DB 10;  Length 1559;
  Best Local Similarity  93.8%;  Pred. No. 1.02e+01;
  Matches    15;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   1301 aggagggcgcacgctg 1316
          |||| ||||||||||
Cp     16 AGGATGGCGCACGCTG 1


RESULT   15
ID   Q56989 standard; DNA; 1559 BP.
AC   Q56989;
DT   12-AUG-1994  (first entry)
DE   Heat-stable carbamylase gene.
KW   Decarbamylase; thermal stability; decarbamylation; heat stable;
KW   N-carbamoyl-D-alpha-aminoacid; point mutation; random mutation;
KW   transformant; E.coli; transform; immobilisation; resin; vector; ds.
OS   Agrobacterium radiobacter.
FH   Key             Location/Qualifiers
FT   CDS             4..915
FT   /*tag= a
FT   /product= heat_stable_carbamylase
PN   WO9403613-A.
PD   17-FEB-1994.
PF   05-AUG-1993; J01101.
PR   10-AUG-1992; JP-212692.
PR   21-DEC-1992; JP-340078.
PA   (KANF ) KANEGAFUCHI KAGAKU KOGYO KK.
PI   Ikenaka Y,  Nanba H,  Takahashi S,  Takano M,  Yajima K;
PI   Yamada Y;
DR   WPI; 94-065701/08.
DR   P-PSDB; R46265.
PT   DNA coding for a decarbamylase with improved thermal stability -
PT   can be used for decarbamylation of
PT   N-carbamoyl-D-alpha-aminoacid(s)
PS   Claim 18; Page 113-115; 177pp; Japanese.
CC   Sequence (Q56963) shows a DNA encoding a thermal stable decarbamylase.
CC   The enzyme's thermo-stability has been improved by modifing the
CC   decarbamylase gene using 'point' and 'random' mutations. These are
CC   shown in sequences (Q56964-92). Sequences (Q56993-996) are also
CC   improved carbamylases contained within various diffrent vectors for
CC   transformation.
SQ   Sequence   1559 BP;    323 A;    476 C;    466 G;    294 T;

  Query Match           77.8%;  Score 14;  DB 10;  Length 1559;
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  Best Local Similarity  93.8%;  Pred. No. 1.02e+01;
  Matches    15;  Conservative    0;  Mismatches   1;  Indels   0;  Gaps   0;

Db   1301 aggagggcgcacgctg 1316
          |||| ||||||||||||
Cp     16 AGGATGGCGCACGCTG 1


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